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        10         20         30         40         50         60         70         80         90
GACGGATCGG GAGATCTGCT AGGTGACCTG AGGGCGGCCG GCTTCGAATA GCCAGAGTAA CCTTTTTTTT TAATTTTATT TTATTTTATT
CTGCCTAGCC CTCTAGACGA TCCACTGGAC TCCGCGCGGC CGAAGCTTAT CGGTCTCATT GGAAAAAAAA ATTAAAATAA AATAAAATAA

       100        110        120        130        140        150        160        170        180
TTTGAGATGG AGTTTGGCGC CGATCTCCCG ATCCCCTATG GTCGACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAGTATC
AAACTCTACC TCAAACCGCG GCTAGAGGGC TAGGGGATAC CAGCTGAGAG TCATGTTAGA CGAGACTACG GCGTATCAAT TCGGTCATAG

       190        200        210        220        230        240        250        260        270
TGCTCCCTGC TTGTGTGTTG GAGGTCGCTG AGTAGTGCGC GAGCAAAATT TAAGCTACAA CAAGGCAAGG CTTGACCGAC AATTGCATGA
ACGAGGGACG AACACACAAC CTCCAGCGAC TCATCACGCG CTCGTTTTAA ATTCGATGTT GTTCCGTTCC GAACTGGCTG TTAACGTACT

       280        290        300        310        320        330        340        350        360
AGAATCTGCT TAGGGTTAGG CGTTTTGCGC TGCTTCGCGA TGTACGGGCC AGATATACGC GTTGACATTG ATTATTGACT AGTTATTAAT
TCTTAGACGA ATCCCAATCC GCAAAAACGCG ACGAAGCGCT ACATGCCCGG TCTATATGCG CAACTGTAAC TAATAACTGA TCAATAATTA

       370        380        390        400        410        420        430        440        450
AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC
TCATTAGTTA ATGCCCCAGT AATCAAGTAT CGGGTATATA CCTCAAGGCG CAATGTATTG AATGCCATTT ACCGGGCGGA CCGACTGGCG

       460        470        480        490        500        510        520        530        540
CCAACGACCC CCGCCCATTG ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA TGGGTGGACT
GGTTGCTGGG GGCGGGTAAC TGCAGTTATT ACTGCATACA AGGGTATCAT TGCGGTTATC CCTGAAAGGT AACTGCAGTT ACCCACCTGA

       550        560        570        580        590        600        610        620        630
ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA AGTACGCCCG CTATTGACGT CAATGACGGT AAATGGCCCG
TAAATGCCAT TTGACGGGTG AACCGTCATG TAGTTCACAT AGTATACGGT TCATGCGGGG GATAACTGCA GTTACTGCCA TTTACCGGGC

       640        650        660        670        680        690        700        710        720
CCTGGCATTA TGCCCAGTAC ATGACCTTAT GGGACTTTCC TATTAGTCAT TACATCTACG CGCTATTACC ATGGTGATGC ..........
GGACCGTAAT ACGGGTCATG TACTGGAATA CCCTGAAAGG ATAATCAGTA ATGTAGATGC GCGATAATGG TACCACTACG ..........

       730        740        750        760        770        780        790        800        810
GGTTTTGGCA GTACATCAAT GGGCGTGGAT CTCACGGGGA TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT ..........
CCAAAACCGT CATGTAGTTA CCCGCACCTA GAGTGCCCCT AAAGGTTCAG AGGTGGGGTA ACTGCAGTTA CCCTCAAACA ..........

       820        830        840        850        860        870        880        890        900
TTTGGCACCA GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA CGGTGGGAGG ..........
AAACCGTGGT CTGAAAGGTT TTACAGCATT GTTGAGGCGG GGTAACTGCG TTTACCCGCC ATCCGCACAT GCCACCCTCC ..........
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FIGURE 14A
(SEQ ID NO. 10)

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 910        920        930        940        950        960        970        980        990
TCTATATAAG CAGAGCTCTC TGGCTAACTA GAGAACCCAC TGCTTACTGG CTTATCGAAA TTAATACGAC TCACTATAGG GAGACCCAAG
AGATATATTC GTCTCGAGAG ACCGATTGAT CTCTTGGGTG ACGAATGACC GAATAGCTTT AATTATGCTG AGTGATATCC CTCTGGGTTC

1000       1010       1020       1030       1040       1050       1060       1070       1080
CTTGGTACCA ATTTAAATTG ATATCTCCTT AGGTCTCGAG TCTCTAGATA ACCGGTCAAT CGATTGGAAT TCTTGCGGCC GCTTGCTAGC
GAACCATGGT TAAATTTAAC TATAGAGGAA TCCAGAGCTC AGAGATCTAT TGGCCAGTTA GCTAACCTTA AGAACGCCGG CGAACGATCG

1090       1100       1110       1120       1130       1140       1150       1160       1170
CACCATGGAG TTGTGGTTAA GCTTGGTCCT TCCTTGTCCT TGTTTTAAAA GGTGTCCAGT GTGAAGTGAA TCTGGTGGAG TCTGGGGGAG
GTGGTACCTC AACACCAATT CGAACCAGGA AGGAACAGGA ACAAAATTTT CCACAGGTCA CACTTCACTT AGACCACCTC AGACCCCCTC

1180       1190       1200       1210       1220       1230       1240       1250       1260
GCTTAGTGCA GCCTGGAGGG TCCCTGAAAG TCTCCTGTGT AACCCTCTGA TTCACTTTCA GTGACTATTA CATGTATTGG GTTCGCCAGA
CGAATCACGT CGGACCTCCC AGGGACTTTC AGAGGACACA TTGGGAGACT AAGTGAAAGT CACTGATAAT GTACATAACC CAAGCGGTCT

1270       1280       1290       1300       1310       1320       1330       1340       1350
CTCCAGAGAA GAGGCTGGAG TGGGTCGCAT ACATTAGTCA AGGTGGTGAT ATAACCGACT ATCCAGACAC TGTAAAGGGT CGATTCACCA
GAGGTCTCTT CTCCGACCTC ACCCAGCGTA TGTAATCAGT TCCACCACTA TATTGGCTGA TAGGTCTGTG ACATTTCCCA GCTAAGTGGT

1360       1370       1380       1390       1400       1410       1420       1430       1440
TCTCCAGAGA CAATGCCAAG AACACCCTGT ACCTGCAAAT GAGCCGTCTG AAGTCTGAGG ACACAGCCAT GTATTACTGT GCAAGAGGCC
AGAGGTCTCT GTTACGGTTC TTGTGGGACA TGGACGTTTA CTCGGCAGAC TTCAGACTCC TGTGTCGGTA CATAATGACA CGTTCTCCGG

1450       1460       1470       1480       1490       1500       1510       1520       1530
TGGACGACGG GGCCTGGTTT GCTTACTGGG GCCAAGGGAC TCTGGTCACG GTCTCTGTAG CTAGCACCAA GGGCCCATCG GTCTTCCCCC
ACCTGCTGCC CCGGACCAAA CGAATGACCC CGGTTCCCTG AGACCAGTGC CAGAGACATC GATCGTGGTT CCCGGGTAGC CAGAAGGGGG

1540       1550       1560       1570       1580       1590       1600       1610       1620
TGGCACCCTC CTCCAAGAGC ACCTCTGGGG GCACAGCGGC CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG ACGGTGTCGT
ACCGTGGGAG GAGGTTCTCG TGGAGACCCC CGTGTCGCCG GGACCCGACG GACCAGTTCC TGATGAAGGG GCTTGGCCAC TGCCACAGCA

1630       1640       1650       1660       1670       1680       1690       1700       1710
GGAACTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTCACCG
CCTTGAGTCC GCGGGACTGG TCGCCGCACG TGTGGAAGGG CCGACAGGAT GTCAGGAGTC CTGAGATGAG GGAGTCGTCG CACCAGTGGC

1720       1730       1740       1750       1760       1770       1780       1790       1800
TGCCCTCCAG CAGCTTGGGC ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA ACACCAGGT  GGACAAGAAA GTTGGTGAGA
ACGGGAGGTC GTCGAACCCG TGGGTCTGGA TGTAGACGTT GCACTTAGTG TTCGGGTCGT TGTGGTCCA  CCTGTTCTTT CAACCACTCT
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FIGURE 14B
(SEQ ID NO. 10)

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        1810       1820       1830       1840       1850       1860       1870       1880       1890
  GGCCAGCACA GGGAGGGAGG GTGTCTGCTG GAAGCCAGGC TCAGGCGCTC TGCCTGGACG CATCCCGGCT ATGCAGCCCC AGTCCAGGGC
  CCGGTCGTGT CCCTCCCTCC CACAGACGAC CTTCGGTCCG AGTCCGCGAG ACGGACCTGC GTAGGGCCGA TACGTCGGGG TCAGGTCCCG

        1900       1910       1920       1930       1940       1950       1960       1970       1980
  AGCAAGGCAG GCCCCGTCTG CCTCTTCACC CGGAGGCCTC TGCCCGCCCC ACTCATGCTC AGGGAGAGGG TCTTCTGGCT TTTTCCCCAG
  TCGTTCCGTC CGGGGCAGAC GGAGAAGTGG GCCTCCGGAG ACGGGCGGGG TGAGTACGAG TCCCTCTCCC AGAAGACCGA AAAAGGGGTC

        1990       2000       2010       2020       2030       2040       2050       2060       2070
  GCTCTGGGCA GGCACAGGCT AGGTGCCCCT AACCCAGGCC CTGCACACAA AGGGGCAGGT GCTGGGCTCA GACCTGCCAA GAGCCATATC
  CGAGACCCGT CCGTGTCCGA TCCACGGGGA TTGGGTCCGG GACGTGTGTT TCCCCGTCCA CGACCCGAGT CTGGACGGTT CTCGGTATAG

        2080       2090       2100       2110       2120       2130       2140       2150       2160
  CGGGAGGACC CTGCCCCTGA CCTAAGCCCA CCCCAAAGGC CAAACTCTCC ACTCCCTCAG CTCGGACACC TTCTCTCCTC CCAGATTCCA
  GCCCTCCTGG GACGGGGACT GGATTCGGGT GGGGTTTCCG GTTTGAGAGG TGAGGGAGTC GAGCCTGTGG AAGAGAGGAG GGTCTAAGGT

        2170       2180       2190       2200       2210       2220       2230       2240       2250
  GTAACTCCCA ATCTTCTCTC TGCAGAGCCC AAATCTTGTG ACAAAACTCA CACATGCCCA CCGTGCCCAG GTAAGCCAGC CCAGGCCTCG
  CATTGAGGGT TAGAAGAGAG ACGTCTCGGG TTTAGAACAC TGTTTTGAGT GTGTACGGGT GGCACGGGTC CATTCGGTCG GGTCCGGAGC

        2260       2270       2280       2290       2300       2310       2320       2330       2340
  CCCTCCAGCT CAAGGGCGGA CAGGTGCCCT AGAGTAGCCT GCATCCAGGG ACACACCACG TGGGTACCAA CATGTCCGGA GCCACATGGA
  GGGAGGTCGA GTTCCGCCCT GTCCACGGGA TCTCATCGGA CGTAGGTCCC TGTGTGGTGC ACCCATGGTT GTACAGGCCT CGGTGTACCT

        2350       2360       2370       2380       2390       2400       2410       2420       2430
  CAGAGGCCGG CTCGGCCCAC CCTCTGCCCT GAGAGTGACC GCTGTACCAA CCTGTGTCCC TACAGGGCAG CCCCGAGAAC CACAGGTGTA
  GTCTCCGGCC GAGCCGGGTG GGAGACGGGA CTCTCACTGG CGACATGGTT GGAGACAGGG ATGTCCCGTC GGGGCTCTTG GTGTCCACAT

        2440       2450       2460       2470       2480       2490       2500       2510       2520
  CACCCTGCCC CCATCCCGGG ATGAGCTGAC CAAGAACCAG GTCAGCCTGA CCTGCCTGGT CAAAGGCTTC TATCCCAGCG ACATCGCCGT
  GTGGGACGGG GGTAGGGCCC TACTCGACTG GTTCTTGGTC CAGTCGGACT GGACGGACCA GTTTCCGAAG ATAGGGTCGC TGTAGCGGCA

        2530       2540       2550       2560       2570       2580       2590       2600       2610
  GGAGTGGGAG AGCAATGGGC AGCCGGAGAA CAACTACAAG ACCACGCCTC CCGTGCTGGA CTCCGACGGC TCCTTCTTCC TCTACAGCAA
  CCTCACCCTC TCGTTACCCG TCGGCCTCTT GTTGATGTTC TGGTGCGGAG GGCACGACCT GAGGCTGCCG AGGAAGAAGG AGATGTCGTT

        2620       2630       2640       2650       2660       2670       2680       2690       2700
  GCTCACCGTG GACAAGAGCA GGTGGCAGCA GGGGAACGTC TTCTCATGCT CCGTGATGCA TGAGGCTCTG CACAACCACT ACACGCAGAA
  CGAGTGGCAC CTGTTCTCGT CCACCGTCGT CCCCTTGCAG AAGAGTACGA GGCACTACGT ACTCCGAGAC GTGTTGGTGA TGTGCGTCTT
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FIGURE 14C
(SEQ ID NO. 10)

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2710       2720       2730       2740       2750       2760       2770       2780       2790
GAGCCCTCTCC CTGTCTCCGG GTAAATGAGT GCGACGGCCG GCAAGCCCCC GCTCCCCGGG CTCTCGCGGT CGCACGAGGA TGCTTGGCAC
CTCGGAGAGG GACAGAGGCC CATTTACTCA CGCTGCCGGC CGTTCGGGGG CGAGGGGCCC GAGAGCGCCA GCGTGCTCCT ACGAACCGTG

2800       2810       2820       2830       2840       2850       2860       2870       2880
GTACCCCCTG TACATACTTC CCGGGGCGCCC AGCATGGAAA TAAAGCACCC AGCGGCTGCCC TGGGCCCCTG CGAGACTGTG ATGGTTCTTT
CATGGGGGAC ATGTATGAAG GGCCCGCGGG TCGTACCTTT ATTTCGTGGG TCGCGACGGG ACCCGGGGAC GCTCTGACAC TACCAAGAAA

2890       2900       2910       2920       2930       2940       2950       2960       2970
CCACGGGGTCA GGCCGAGTCT GAGGCCTGAG TGGCATGAGG GAGGCAGAGC GGGTCCCACT GTCCCCACAC TGGCCCAGGC TGTGCAGGTG
GGTGCCCAGT CCGGCTCAGA CTCCGGACTC ACCGTACTCC CTCCGTCTCG CCCAGGGTGA CAGGGGTGTG ACCGGGTCCG ACACGTCCAC

2980       2990       3000       3010       3020       3030       3040       3050       3060
TGCCTGGGCC CCCTAGGGTG GGGCTCAGCC AGGGGCTGCC CTCGGCAGGG TGGGGGATTT GCCAGCGTGG CCCTCCCTCC AGCAGCACCT
ACGGACCCGG GGGATCCCAC CCCGAGTCGG TCCCCGACGG GAGCCGTCCC ACCCCCTAAA CGGTCGCACC GGGAGGGAGG TCGTCGTGA

3070       3080       3090       3100       3110       3120       3130       3140       3150
GCCCTGGGCT GGGCCACGGG AAGCCCTAGG AGCCCCTGGG GACAGACACA CAGCCCCTGC CTCTGTAGGA GACTGTCCTG TTCTGTGAGC
CGGGACCCGA CCCGGTGCCC TTCGGGATCC TCGGGGACCC CTGTCTGTGT GTCGGGGACG GAGACATCCT CTGACAGGAC AAGACACTCG

3160       3170       3180       3190       3200       3210       3220       3230       3240
GCCCCTGTCC TCCCGACCTC CATGCCCACT CGGGGGGCATG GTGCGTAGGG ACAGGCCCTC ACAGGCCCTC CCTCACCCAT CTACCCCCAC
CGGGACAGG AGGGCTGGAG GTACGGGTGA GCCCCCGTAC GGATCAGGTA CACGCATCCC TGTCCGGGAG GGAGTGGGTA GATGGGGGTG

3250       3260       3270       3280       3290       3300       3310       3320       3330
GGCACTAAACC CCTGGCTGCC CTGCCCAGCC TCGCACCCGC ATGGGGACAC AACCGACTCC GGGGACATGC ACTCTCGGGC CCTGTGGAGG
CCGTGATTGG GGACCGACGG GACGGGTCGG AGCGTGGGCG TACCCCTGTG TTGGCTGAGG CCCCTGTACG TGAGAGCCCG GGACACCTCC

3340       3350       3360       3370       3380       3390       3400       3410       3420
GACTGGTGCA GATGCCCACA CACACACTCA GCCCAGACCC GTTCAACAAA CCCCGCACTG AGGTTGGCCG GCCACACGGC CACCACACAC
CTGACCACGT CTACGGGTGT GTGTGTGAGT CGGGTCTGGG CAAGTTGTTT GGGGCGTGAC TCCAACGGC CGGTGTGCCG GTGGTGTGTG

3430       3440       3450       3460       3470       3480       3490       3500       3510
ACACGTGCAC GCCTCACACA CGGAGCCTCA CCCGGGCGAA CTGCACAGCA CCCAGACCAG AGCAAGGTCC TCGCACACGT GAACACTTCT
TGTGCACGTG CGGAGTGTGT GCCTCGGAGT GGGCCCGCTT GACGTGTCGT GGGTCTGGTC TCGTTCCAGG AGCGTGTGCA CTTGTGAGGA

3520       3530       3540       3550       3560       3570       3580       3590       3600
CGGACACAGG CCCCACGCGG CACCTCAAGG CCCACGAGCC TCTCGGCAGC TTCTCCACAT GCTGACCTGC TCAGACAAAC TCAGACAAAC
GCCTGTGTCC GGGGGTGCTC GTGGAGTTCC GGGTGCTCGG AGAGCCGTCG AAGAGGTGTA CGACTGGACG AGTCTGTTTG
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FIGURE 14D
(SEQ ID NO. 10)

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      3610       3620       3630       3640       3650       3660       3670       3680       3690
CCAGCCCTCC TCTCACAAGG GTGCCCCTGC AGCCGCCACA CACACACAGG GGATCACACA CCACGTCACG TCCCTGGCCC TGGCCCACTT
GGTCGGGAGG AGAGTGTTCC CACGGGGACG TCGGCGGTGT GTGTGTGTCC CCTAGTGTGT GGTGCAGTGC AGGGACCGGG ACCGGGTGAA

      3700       3710       3720       3730       3740       3750       3760       3770       3780
CCCAGTGCCG CCCTTCCCTG CAGGACGGAT CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC CATCTGTTGT TTGCCCCTCC CCCGTGCCTT
GGGTCACGGC GGGAAGGGAC GTCCTGCCTA GTCGGAGCTG ACACGGAAGA TCAACGGTCG GTAGACAACA AACGGGGAGG GGGCACGGAA

      3790       3800       3810       3820       3830       3840       3850       3860       3870
CCTTGACCCT GGAAGGTGCC ACTCCCACTG TCCTTTCCTA ATAAAATGAG GAAATTGCAT CGCATTGCAT GAGTAGGTGT CATTCTATTC
GGAACTGGGA CCTTCCACGG TGAGGGTGAC AGGAAAGGAT TATTTTACTC CTTTAACGTA GCGTAACGTA CTCATCCACA GTAAGATAAG

      3880       3890       3900       3910       3920       3930       3940       3950       3960
TGGGGGGTGG GGTGGGGCAG GACAGCAAGG GGGAGGATTG GGAAGACAAT AGCAGGCATG CTGGGGATGC GGTGGGCTCT ATGGCTTCTG
ACCCCCCACC CCACCCCGTC CTGTCGTTCC CCCTCCTAAC CCTTCTGTTA TCGTCCGTAC GACCCCTACG CCACCCGAGA TACCGAAGAC

      3970       3980       3990       4000       4010       4020       4030       4040       4050
AGGCGGAAAG AACCAGCTGG GGCTCTAGGG GGTATCCCCA CGGCCCCTGT AGCGGCGCAT TAAGCGCGGC GGGTGTGGTG GTTACGGGCA
TCCGCCTTTC TTGGTCGACC CCGAGATCCC CCATAGGGGT GCCGGGGACA TCGCCGCGTA ATTCGCGCCG CCCACACCAC CAATGCGCGT

      4060       4070       4080       4090       4100       4110       4120       4130       4140
GCGTGACCGC TACACTTGCC AGCGCCCTAG CGCCCGCTCC TTTCGCTTTC TTCCCTTCCT TTCTCGCCAC GTTCGCGGGG CCTCTCAAAA
CGCACTGGCG ATGTGAACGG TCGCGGGATC GCGGGCGAGG AAAGCGAAAG AAGGGAAGGA AAGAGCGGTG CAAGCGCCCC GGAGAGTTTT

      4150       4160       4170       4180       4190       4200       4210       4220       4230
AAGGGAAAAA AAGCATGCAT CTCAATTAGT CAGCAACCAT AGTCCCGCCC CCATCCCGCC CTAACTCCGC CCTAACTCCG CCCAGTTCCG
TTCCCTTTTT TTCGTACGTA GAGTTAATCA GTCGTTGGTA TCAGGGCGGG GGTAGGGCGG GATTGAGGCG GGATTGAGGC GGGTCAAGGC

      4240       4250       4260       4270       4280       4290       4300       4310       4320
CCCATTCTCC GCCCCATGGC TGACTAATTT TTTTATTTTA TGCAGAGGCC GAGGCCGCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG
GGGTAAGAGG CGGGGTACCG ACTGATTAAA AAAATAAAAT ACGTCTCCGG CTCCGGCGGA GCCGGAGACT CGATAAGGTC TTCATCACTC

      4330       4340       4350       4360       4370       4380       4390       4400       4410
GAGGCTTTTT TGGAGGCCTA GGCTTTTGCA AAAAGCTTGG ACAGCTCAGG GCTGCGATTT CGGCCCAAAC TTGACGGCAA TCCTAGCGTG
CTCCGAAAAA ACCTCCGGAT CCGAAAACGT TTTTCGAACC TGTCGAGTCC CGACGCTAAA GCCGGGTTTG AACTGCCGTT AGGATCGCAC

      4420       4430       4440       4450       4460       4470       4480       4490       4500
AAGGCTGGTA GGATTTTATC CCTGCTGCCA TCATGGTTCG ACCAATGAAC TGCATCGTCG CCGTGTCCCA AAATATGGGG ATTGGCAAGA
TTCCGACCAT CCTAAAATAG GGACGACGGT AGTACCAAGC TGGTTACTTG ACGTAGCAGC GGCACAGGGT TTTATACCCC TAACCGTTCT
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FIGURE 14E
(SEQ ID NO. 10)

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4510        4520        4530        4540        4550        4560        4570        4580        4590
ACCGGAGACCT ACCCTGCCCT  CCGCTCAGGA  ACGAGTTCAA  GTACTTCCAA  AGAATGACCA  CAACCTCTTC  AGTGGAAGGT  AAACAGAATC
TGCCTCTGGA  TGGGACCGGA  GGCGAGTCCT  TGCTCAAGTT  CATGAAGGTT  TCTTACTGGT  GTTGGAGAAG  TCACCTTCCA  TTTGTCTTAG

4600        4610        4620        4630        4640        4650        4660        4670        4680
TGGTGATTAT  GGGTAGGAAA  ACCTGGTTCT  CCATTCCTGA  GAAGAATCGA  CCTTTAAAGG  ACAGAATTAA  TATAGTTCTC  AGTAGAGAAC
ACCACTAATA  CCCATCCTTT  TGGACCAAGA  GGTAAGGACT  CTTCTTAGCT  GGAAATTTCC  TGTCTTAATT  ATATCAAGAG  TCATCTCTTG

4690        4700        4710        4720        4730        4740        4750        4760        4770
TCAAAGAACC  ACCACGAGGA  GCTCATTTTC  TTGCCAAAAG  GCCTTAAGAC  TTATTGAACA  ACCGGAATTG  GCAAGTAAAG
AGTTCTTTGG  TGGTGCTCCT  CGAGTAAAAG  AACGGTTTTC  CGGAATTCTG  AATAACTTGT  TGGCCTTAAC  CGTTCATTTC

4780        4790        4800        4810        4820        4830        4840        4850        4860
TAGACATGGT  TTGGATAGTC  GGAGGCAGTT  CTGTTTACCA  GGAAGCCATG  AATCAACCAG  GCCACCTTAG  ACTCTTTGTG  ACAAGGATCA
ATCTGTACCA  AACCTATCAG  CCTCCGTCAA  GACAAATGGT  CCTTCGGTAC  TTAGTTGGTC  CGGTGGAATC  TGAGAAACAC  TGTTCCTAGT

4870        4880        4890        4900        4910        4920        4930        4940        4950
TGCAGGAATT  TGAAAGTGAC  ACGTTTTTCC  CAGAAATTGA  TTTGGGGAAA  TATAAACTTC  TCCCAGAATA  CCCAGCCGTC  CTCTCTGAGG
ACGTCCTTAA  ACTTTCACTG  TGCAAAAAGG  GTCTTTAACT  AAACCCCTTT  ATATTTGAAG  AGGGTCTTAT  GGGTCGGCAG  GAGAGACTCC

4960        4970        4980        4990        5000        5010        5020        5030        5040
TCCAGGAGGA  AAAAGGCATC  AAGTATAAGT  TTGAAGTCTA  CGAGAAGAAA  GACTAACAGG  AAGATGCTTT  CAAGTTCTCT  GCTCCCCTCC
AGGTCCTCCT  TTTTCCGTAG  TTCATATTCA  AACTTCAGAT  GCTCTTCTTT  CTGATTGTCC  TTCTACGAAA  GTTCAAGAGA  CGAGGGGAGG

5050        5060        5070        5080        5090        5100        5110        5120        5130
TAAAGCTATG  CATTTTTATA  AGACCATGGG  ACTTTTGCTG  GCTTTAGATC  TCTTTGTGAA  GGAACCTTAC  TTCTGTGGTG  TGACATAATT
ATTTCGATAC  GTAAAAATAT  TCTGGTACCC  TGAAAACGAC  CGAAATCTAG  AGAAACACTT  CCTTGGAATG  AAGACACCAC  ACTGTATTAA

5140        5150        5160        5170        5180        5190        5200        5210        5220
GGACAAACTA  CCTACAGAGA  TTTAAAGCTC  TAAGGTAAAT  ATAAAATTTT  TAAGTGTATA  ATGTGTTAAA  CTACTGATTC  TAATTGTTTG
CCTGTTTGAT  GGATGTCTCT  AAATTTCGAG  ATTCCATTTA  TATTTTAAAA  ATTCACATAT  TACACAATTT  GATGACTAAG  ATTAACAAAC

5230        5240        5250        5260        5270        5280        5290        5300        5310
TGTATTTTAG  ATTCCAACCT  ATGGAACTGA  TGAATGGGAG  CAGTGGTGGA  ATGCCTTTAA  TGAGGAAAAC  CTGTTTTGCT  CAGAAGAAAT
ACATAAAATC  TAAGGTTGGA  TACCTTGACT  ACTTACCCTC  GTCACCACCT  TACGGAAATT  ACTCCTTTTG  GACAAAACGA  GTCTTCTTTA

5320        5330        5340        5350        5360        5370        5380        5390        5400
GCCATCTAGT  GATGATGAGG  CTACTGCTGA  CTCTCAACAT  TCTACTCCTC  CAAAAAAGAA  GAGAAAGGTA  GAAGACCCCA  AGGACTTTCC
CGGTAGATCA  CTACTACTCC  GATGACGACT  GAGAGTTGTA  AGATGAGGAG  GTTTTTTCTT  CTCTTTCCAT  CTTCTGGGGT  TCCTGAAAGG
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FIGURE 14F
(SEQ ID NO. 10)

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5410        5420        5430        5440        5450        5460        5470        5480        5490
TTCAGAATTG  CTAAGTTTTT  TGAGTCATGC  TGTGTTTAGT  AATAGAACTC  TTGCTTGCTT  TGCTATTTAC  ACCACAAAGG  AAAAAGCTGC
AAGTCTTAAC  GATTCAAAAA  ACTCAGTACG  ACACAAATCA  TTATCTTGAG  AACGAACGAA  ACGATAAATG  TGGTGTTTCC  TTTTTCGACG

5500        5510        5520        5530        5540        5550        5560        5570        5580
ACTGCTATAC  AAGAAAATTA  TGGAAAAATA  TTCTGTAACC  TTTATAAGTA  GGCATAACAG  TTATAATCAT  AACATACTGT  TTTTTCTTAC
TGACGATATG  TTCTTTTAAT  ACCTTTTTAT  AAGACATTGG  AAATATTCAT  CCGTATTGTC  AATATTAGTA  TTGTATGACA  AAAAAGAATG

5590        5600        5610        5620        5630        5640        5650        5660        5670
TCCACACAGG  CATAGAGTGT  CTGCTATTAA  TAACTATGCT  CAAAAATTGT  GTACCTTTAG  CTTTTTAATT  TGTAAAGGGG  TTAATAAGGA
AGGTGTGTCC  GTATCTCACA  GACGATAATT  ATTGATACGA  GTTTTTAACA  CATGGAAATC  GAAAAATTAA  ACATTTCCCC  AATTATTCCT

5680        5690        5700        5710        5720        5730        5740        5750        5760
ATATTTGATG  TATAGTGCCT  TGACTAGAGA  TCATAATCAG  CCATACCACA  TTTGTAGAGG  TTTTACTTGC  TTTAAAAAAC  CTCCCACACC
TATAAACTAC  ATATCACGGA  ACTGATCTCT  AGTATTAGTC  GGTATGGTGT  AAACATCTCC  AAAATGAACG  AAATTTTTTG  GAGGGTGTGG

5770        5780        5790        5800        5810        5820        5830        5840        5850
TCCCCCTGAA  CCTGAAACAT  AAAATGAATG  CAATTGTTGT  TGTTAACTTG  TTTATTGCAG  CTTATAATGG  TTACAAATAA  AGCAATAGCA
AGGGGGACTT  GGACTTTGTA  TTTTACTTAC  GTTAACAACA  ACAATTGAAC  AAATAACGTC  GAATATTACC  AATGTTTATT  TCGTTATCGT

5860        5870        5880        5890        5900        5910        5920        5930        5940
TCACAAATTT  CACAAATAAA  GCATTTTTTT  CACTGCATTC  TAGTTGTGGT  TTGTCCAAAC  TCATCAATGT  ATCTTATCAT  GTCTCGATCG
AGTGTTTAAA  GTGTTTATTT  CGTAAAAAAA  GTGACGTAAG  ATCAACACCA  AACAGGTTTG  AGTAGTTACA  TAGAATAGTA  CAGAGCTAGC

5950        5960        5970        5980        5990        6000        6010        6020        6030
GCTGGATGAT  CCTCCAGCGC  GGGGATCTCA  TGCTGGAGTT  CTTCGCCCAC  CCCAACTTGT  TTATTGCAGC  TTATAATGGT  TACAAATAAA
CGACCTACTA  GGAGGTCGCG  CCCCTAGAGT  ACGACCTCAA  GAAGCGGGTG  GGGTTGAACA  AATAACGTCG  AATATTACCA  ATGTTTATTT

6040        6050        6060        6070        6080        6090        6100        6110        6120
GCAATAGCAT  CACAAATTTC  ACAAATAAAG  CATTTTTTTC  ACTGCATTCT  AGTTGTGGTT  TGTCCAAACT  CATCAATGTA  TCTTATCATG
CGTTATCGTA  GTGTTTAAAG  TGTTTATTTC  GTAAAAAAAG  TGACGTAAGA  TCAACACCAA  ACAGGTTTGA  GTAGTTACAT  AGAATAGTAC

6130        6140        6150        6160        6170        6180        6190        6200        6210
TCTGTATACC  GTCGACCTCT  AGCTAGAGCT  TGGCGTAATC  ATGGTCATAG  CTGTTTCCTG  TGTGAAATTG  TTATCCGCTC  ACAATTCCAC
AGACATATGG  CAGCTGGAGA  TCGATCTCGA  ACCGCATTAG  TACCAGTATC  GACAAAGGAC  ACACTTTAAC  AATAGGCGAG  TGTTAAGGTG

6220        6230        6240        6250        6260        6270        6280        6290        6300
ACAACATACG  AGCCGGAAGC  ATAAAGTGTA  AAGCCTGGGG  TGCCTAATGA  GTGAGCTAAC  TCACATTAAT  TGCGTTGCGC  TCACTGCCCG
TGTTGTATGC  TCGGCCTTCG  TATTTCACAT  TTCGGACCCC  ACGGATTACT  CACTCGATTG  AGTGTAATTA  ACGCAACGCG  AGTGACGGGC
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FIGURE 14G
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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    6310        6320        6330        6340        6350        6360        6370        6380        6390
CTTTCCAGTC  TCGTGCCAGC  TGCATTAATG  AATCGGCCAA  CGCGCGGGGA  GAGGCGGTTT  GGTTATTGGG  CGCTCTTCCG
GAAAGGTCAG  AGCACGGTCG  ACGTAATTAC  TTAGCCGGTT  GCGCGCCCCT  CTCCGCCAAA  CGCATAACCC  GCGAGAAGGC

    6400        6410        6420        6430        6440        6450        6460        6470        6480
CTTCCTCGCT  CACTGACTCG  CTGCGCTCGG  TCGTTCGGCT  GCGGCGAGCG  GTATCAGCTC  ACTCAAAGGC  GGTAATACGG  TTATCCACAG
GAAGGAGCGA  GTGACTGAGC  GACGCGAGCC  AGCAAGCCGA  CGCCGCTCGC  CATAGTCGAG  TGAGTTTCCG  CCATTATGCC  AATAGGTGTC

    6490        6500        6510        6520        6530        6540        6550        6560        6570
AATCAGGGGA  TAACGCCAGA  AAGAACATGT  GAGCAAAAGG  CCAGCAAAAG  GCCAGGAACC  GTAAAAAGGC  CGCGTTGCTG  GCGTTTTTCC
TTAGTCCCCT  ATTGCGGTCT  TTCTTGTACA  CTCGTTTTCC  GGTCGTTTTC  CGGTCCTTGG  CATTTTTCCG  GCGCAACGAC  CGCAAAAAGG

    6580        6590        6600        6610        6620        6630        6640        6650        6660
ATAGGCTCCG  CCCCCCTGAC  GAGCATCACA  AAAATCGACG  CTCAAGTCAG  AGGTGGCGAA  ACCCGACAGG  ACTATAAAGA  TACCAGGCGT
TATCCGAGGC  GGGGGGACTG  CTCGTAGTGT  TTTTAGCTGC  GAGTTCAGTC  TCCACCGCTT  TGGGCTGTCC  TGATATTTCT  ATGGTCCGCA

    6670        6680        6690        6700        6710        6720        6730        6740        6750
TTCCCCCTGG  AAGCTCCCTC  GTGCGCTCTC  CTGTTCCGAC  CCTGCCGCTT  ACCGGATACC  TGTCCGCCTT  TCTCCCTTCG  GGAAGCGTGG
AAGGGGGACC  TTCGAGGGAG  CACGCGAGAG  GACAAGGCTG  GGACGGCGAA  TGGCCTATGG  ACAGGCGGAA  AGAGGGAAGC  CCTTCGCACC

    6760        6770        6780        6790        6800        6810        6820        6830        6840
CGCTTTCTCA  ATGCTCACGC  TGTAGGTATC  TCAGTTCGGT  GTAGGTCGTT  CGCTCCAAGC  TGGGCTGTGT  GCACGAACCC  CCCGTTCAGC
GCGAAAGAGT  TACGAGTGCG  ACATCCATAG  AGTCAAGCCA  CATCCAGCAA  GCGAGGTTCG  ACCCGACACA  CGTGCTTGGG  GGGCAAGTCG

    6850        6860        6870        6880        6890        6900        6910        6920        6930
CCGACCGCTG  CGCCTTATCC  GGTAACTATC  GTCTTGAGTC  CAACCCGGTA  AGACACGACT  TATCGGCCACT GGCAGCAGCC  ACTGGTAACA
GGCTGGCGAC  GCGGAATAGG  CCATTGATAG  CAGAACTCAG  GTTGGGCCAT  TCTGTGCTGA  ATAGCGGTGA  CCGTCGTCGG  TGACCATTGT

    6940        6950        6960        6970        6980        6990        7000        7010        7020
GGATTAGCAG  AGCGAGGTAT  GTAGGCGGTG  CTACAGAGTT  CTTGAAGTGG  TGGCCTAACT  ACGGCTACAC  TAGAAGGACA  GTATTTGGTA
CCTAATCGTC  TCGCTCCATA  CATCCGCCAC  GATGTCTCAA  GAACTTCACC  ACCGGATTGA  TGCCGATGTG  ATCTTCCTGT  CATAAACCAT

    7030        7040        7050        7060        7070        7080        7090        7100        7110
TCTGCGCTCC- GCTGAAGCCA  GTTACCTTCG  GAAAAAGAGT  TGGTAGCTCT  TGATCCGGCA  AACAAACCAC  CGCTGGTAGC  GGTGGTTTTT
AGACGCGAGA  CGACTTCGGT  CAATGGAAGC  CTTTTTCTCA  ACCATCGAGA  ACTAGGCCGT  TTGTTTGGTG  GCGACCATCG  CCACCAAAAA

    7120        7130        7140        7150        7160        7170        7180        7190        7200
TTGTTTGCAA  GCAGCAGATT  ACGCGCAGAA  AAAAAGGATC  TCAAGAAGAT  CCTTTGATCT  TTTCTACGGG  GTCTGACGCT  CAGTGGAACG
AACAAACGTT  CGTCGTCTAA  TGCGCGTCTT  TTTTTCCTAG  AGTTCTTCTA  GGAAACTAGA  AAAGATGCCC  CAGACTGCGA  GTCACCTTGC
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FIGURE 14H
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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        7210       7220       7230       7240       7250       7260       7270       7280       7290
  AAAACTCACG TTAAGGGATT GATTATCAAGA AAGGATCTTC ACCTAGATCC TTTTAAATTA AAAATTTAAT AAAATGAAGT TTTAAATCAA
  TTTTGAGTGC AATTCCCTAA CTAATAGTACT TTCCTAGAAG TGGATCTAGG AAAATTTAAT TTTTAAATTA TTTTACTTCA AAATTTAGTT

        7300       7310       7320       7330       7340       7350       7360       7370       7380
  TCTAAAGTAT ATATGAGTAA ACTTGGTCTG ACAGTTACCA ATGCTTAATC AGTGAGGCAC CTATCTCAGC GATCTGTCTA TTTCGTTCAT
  AGATTTCATA TATACTCATT TGAACCAGAC TGTCAATGGT TACGAATTAG TCACTCCGTG GATAGAGTCG CTAGACAGAT AAAGCAAGTA

        7390       7400       7410       7420       7430       7440       7450       7460       7470
  CCATAGTTGC CTGACTCCCC GTCGTGTAGA TAACTACGAT ACGGGAGGGC TTACCATCTG GCCCCAGTGC TGCAATGATA CCGCGAGACC
  GGTATCAACG GACTGAGGGG CAGCACATCT ATTGATGCTA TGCCCTCCCG AATGGTAGAC CGGGGTCACG ACGTTACTAT GGCGCTCTGG

        7480       7490       7500       7510       7520       7530       7540       7550       7560
  CACGCTCACC GGCTCCAGAT TTATCAGCAA TAAACCAGCC AGCCGGAAGG GCCGAGCGCA GAAGTGGTCC TGCAACTTTA TCCGCCTCCA
  GTGCGAGTGG CCGAGGTCTA AATAGTCGTT ATTTGGTCGG TCGGCCTTCC CGGCTCGCGT CTTCACCAGG ACGTTGAAAT AGGCGGAGGT

        7570       7580       7590       7600       7610       7620       7630       7640       7650
  TCCAGTCTAT TAATTGTTGC CGGGAAGCTA GAGTAAGTAG TTCGCCAGTT AATAGTTTGC GCAACGTTGT TGCCATTGCT ACAGGCATCG
  AGGTCAGATA ATTAACAACG GCCCTTCGAT CTCATTCATC AAGCGGTCAA TTATCAAACG CGTTGCAACA ACGGTAACGA TGTCCGTAGC

        7660       7670       7680       7690       7700       7710       7720       7730       7740
  TGGTGTCACG CTCGTCGTTT GGTATGGCTT CATTCAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG ATCCCCCATG TTGTGCAAAA
  ACCACAGTGC GAGCAGCAAA CCATACCGAA GTAAGTCGAG GCCAAGGGTT GCTAGTTCCG CTCAATGTAC TAGGGGGTAC AACACGTTTT

        7750       7760       7770       7780       7790       7800       7810       7820       7830
  AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAGAAG TAAGTTGGCC GCAGTGTTAT CACTCATGGT TATGGCAGCA CTGCATAATT
  TTCGCCAATC GAGGAAGCCA GGAGGCTAGC AACAGTCTTC ATTCAACCGG CGTCACAATA GTGAGTACCA ATACCGTCGT GACGTATTAA

        7840       7850       7860       7870       7880       7890       7900       7910       7920
  CTCTTACTGT CATGCCATCC GTAAGATGCT TTTCTGTGAC TGGTGAGTAC TCAACCAAGT CATTCTGAGA ATAGTGTATG CGGCGACCGA
  GAGAATGACA GTACGGTAGG CATTCTACGA AAAGACACTG ACCACTCATG AGTTGGTTCA GTAAGACTCT TATCACATAC GCCGCTGGCT

        7930       7940       7950       7960       7970       7980       7990       8000       8010
  GTTGCTCTTG CCCGGCGTCA ATACGGGATA ATACCGCGCC ACATAGCAGA ACTTTAAAAG TGCTCATCAT TGGAAAACGT TCTTCGGGGC
  CAACGAGAAC GGGCCGCAGT TATGCCCTAT TATGGCGCGG TGTATCGTCT TGAAATTTTC ACGAGTAGTA ACCTTTTGCA AGAAGCCCCG

        8020       8030       8040       8050       8060       8070       8080       8090       8100
  GAAAACTCTC AAGGATCTTA CCGCTGTTGA GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC TTCAGCATCT TTTACTTTCA
  CTTTTGAGAG TTCCTAGAAT GGCGACAACT CTAGGTCAAG CTACATTGGG TGAGCACGTG GGTTGACTAG AAGTCGTAGA AAATGAAAGT
```

FIGURE 14I
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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        8110       8120       8130       8140       8150       8160       8170       8180       8190
CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAG GGAATAAGGG CGACACGGAA ATGTTGAATA CTCATACTCT
GGTCGCAAAG ACCCACTCGT TTTTGTCCTT CCGTTTTTACG GCGTTTTTTC CCTTATTCCC GCTGTGCCTT TACAACTTAT GAGTATGAGA

        8200       8210       8220       8230       8240       8250       8260       8270       8280
TCCTTTTTCA ATATTATTGA AGCATTTATC AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG
AGGAAAAAGT TATAATAACT TCGTAAATAG TCCCAATAAC AGAGTACTCG CCTATGTATA AACTTACATA AATCTTTTTA TTTGTTTATC

        8290       8300       8310       8320       8330
GGGTTCCGCG CACATTTCCC CGAAAAGTGC CACCTGACGT C
CCCAAGGCGC GTGTAAAGGG GCTTTTCACG GTGGACTGCA G
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FIGURE 14J
SEQ ID NO. 10)

FIGURE 18A (SEQ ID NO. 22)

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   1  GGTACCAATT  TAAATTGATA  TCTCCTTAGG  TCTCGAGTCT  CTAGATAACC

  51  GGTCAATCGA  TTGGAATTCT  TGCGGCCGCT  TGCTAGCCAC  CATGGAGTTG

 101  TGGTTAAGCT  TGGTCTTCCT  TGTCCTTGTT  TTAAAAGGTG  TCCAGTGTGA

 151  AGTGCAACTG  GTGGAGTCTG  GGGGAGGCTT  AGTGCAGCCT  GGAGGGTCCC

 201  TGCGACTTTC  CTGTGCTGCA  TCTGGATTCC  CGTTCAGTGA  CTATTACATG

 251  TATTGGGTTC  GCCAGGCTCC  AGGCAAGGGA  CTGGAGTGGG  TCTCATACAT

 301  TAGTCAAGAT  GGTGATATAA  CCGACTATGC  AGACTCCGTA  AAGGGTCGAT

 351  TCACCATCTC  CAGAGACAAT  GCAAAGAACA  GCCTGTACCT  GCAAATGAAC

 401  AGCCTGAGGG  ACGAGGACAC  AGCCGTGTAT  TACTGTGCAA  GAGGCCTGGC

 451  GGACGGGGCC  TGGTTTGCTT  ACTGGGGCCA  AGGGACTCTG  GTCACGGTCT

 501  CTTCCGCTAG  CACCAAGGGC  CCATCGGTCT  TCCCCCTGGC  ACCCTCCTCC

 551  AAGAGCACCT  CTGGGGGCAC  AGCGGCCCTG  GGCTGCCTGG  TCAAGGACTA

 601  CTTCCCCGAA  CCGGTGACGG  TGTCGTGGAA  CTCAGGCGCC  CTGACCAGCG

 651  GCGTGCACAC  CTTCCCGGCT  GTCCTACAGT  CCTCAGGACT  CTACTCCCTC

 701  AGCAGCGTGG  TCACCGTGCC  CTCCAGCAGC  TTGGGCACCC  AGACCTACAT

 751  CTGCAACGTG  AATCACAAGC  CCAGCAACAC  CAAGGTGGAC  AAGAAAGTTG

 801  GTGAGAGGCC  AGCACAGGGA  GGGAGGGTGT  CTGCTGGAAG  CCAGGCTCAG

 851  CGCTCCTGCC  TGGACGCATC  CCGGCTATGC  AGCCCCAGTC  CAGGGCAGCA

 901  AGGCAGGCCC  CGTCTGCCTC  TTCACCCGGA  GGCCTCTGCC  CGCCCCACTC

 951  ATGCTCAGGG  AGAGGGTCTT  CTGGCTTTTT  CCCCAGGCTC  TGGGCAGGCA

1001  CAGGCTAGGT  GCCCCTAACC  CAGGCCCTGC  ACACAAAGGG  GCAGGTGCTG

1051  GGCTCAGACC  TGCCAAGAGC  CATATCCGGG  AGGACCCTGC  CCCTGACCTA

1101  AGCCCACCCC  AAAGGCCAAA  CTCTCCACTC  CCTCAGCTCG  GACACCTTCT

1151  CTCCTCCCAG  ATTCCAGTAA  CTCCCAATCT  TCTCTCTGCA  GAGCCCAAAT

1201  CTTGTGACAA  AACTCACACA  TGCCCACCGT  GCCCAGGTAA  GCCAGCCCAG

1251  GCCTCGCCCT  CCAGCTCAAG  GCGGGACAGG  TGCCCTAGAG  TAGCCTGCAT

1301  CCAGGGACAG  GCCCCAGCCG  GGTGCTGACA  CGTCCACCTC  CATCTCTTCC
```

1351 TCAGCACCTG AACTC[CTG]GG G[GGA]CCGTCA GTCTTCCTCT TCCCCCCAAA

1401 ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG

1451 TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG

1501 GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA

1551 CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT

1601 GGCTGAATGG CAAG[GAG]TAC [AAG]TGC[AAG]G TCTCCAACAA AGCCCTCCCA

1651 GCC[CCC]ATCG AGAAAACCAT CTCCAAAGCC AAAGGTGGGA CCCGTGGGGT

1701 GCGAGGGCCA CATGGACAGA GGCCGGCTCG GCCCACCCTC TGCCCTGAGA

1751 GTGACCGCTG TACCAACCTC TGTCCCTACA GGGCAGCCCC ·GAGAACCACA

1801 GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG AACCAGGTCA

1851 GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG

1901 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT

1951 GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA

2001 AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG

2051 GCTCTGCACA ACCACTACAC GCAGAAGAGC CTCTCCCTGT CTCCGGGTAA

2101 ATGAGTGCGA CGGCCGGCAA GCCCCCGCTC CCCGGGCTCT CGCGGTCGCA

2151 CGAGGATGCT TGGCACGTAC CCCCTGTACA TACTTCCCGG GCGCCCAGCA

2201 TGGAAATAAA GCACCCAGCG CTGCCCTGGG CCCCTGCGAG ACTGTGATGG

2251 TTCTTTCCAC GGGTCAGGCC GAGTCTGAGG CCTGAGTGGC ATGAGGGAGG

2301 CAGAGCGGGT CCCACTGTCC CCACACTGGC CCAGGCTGTG CAGGTGTGCC

2351 TGGGCCCCCT AGGGTGGGGC TCAGCCAGGG CTGCCCTCG GCAGGGTGGG

2401 GGATTTGCCA GCGTGGCCCT CCCTCCAGCA GCACCTGCCC TGGGCTGGGC

2451 CACGGGAAGC CCTAGGAGCC CCTGGGGACA GACACACAGC CCCTGCCTCT

2501 GTAGGAGACT GTCCTGTTCT GTGAGCGCCC CTGTCCTCCC GACCTCCATG

2551 CCCACTCGGG GGCATGCCTA GTCCATGTGC GTAGGGACAG GCCCTCCCTC

2601 ACCCATCTAC CCCCACGGCA CTAACCCCTG GCTGCCCTGC CCAGCCTCGC

2651 ACCCGCATGG GGACACAACC GACTCCGGGG ACATGCACTC TCGGGCCCTG

2701 TGGAGGGACT GGTGCAGATG CCCACACACA CACTCAGCCC AGACCCGTTC

2751 AACAAACCCC GCACTGAGGT TGGCCGGCCA CACGGCCACC ACACACACAC

2801 GTGCACGCCT CACACACGGA GCCTCACCCG GGCGAACTGC ACAGCACCCA

FIGURE 18B (SEQ ID NO. 22)

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2851   GACCAGAGCA   AGGTCCTCGC   ACACGTGAAC   ACTCCTCGGA   CACAGGCCCC

2901   CACGAGCCCC   ACGCGGCACC   TCAAGGCCCA   CGAGCCTCTC   GGCAGCTTCT

2951   CCACATGCTG   ACCTGCTCAG   ACAAACCCAG   CCCTCCTCTC   ACAAGGGTGC

3001   CCCTGCAGCC   GCCACACACA   CACAGGGGAT   CACACACCAC   GTCACGTCCC

3051   TGGCCCTGGC   CCACTTCCCA   GTGCCGCCCT   TCCCTGCAGG   ACGGATCAGC

3101   CTCGACTGTG   CCTTCTAGTT   GCCAGCCATC   TGTTGTTTGC   CCCTCCCCCG

3151   TGCCTTCCTT   GACCCTGGAA   GGTGCCACTC   CCACTGTCCT   TTCCTAATAA

3201   AATGAGGAAA   TTGCATCGCA   TTGTCTGAGT   AGGTGTCATT   CTATTCTGGG

3251   GGGTGGGGTG   GGGCAGGACA   GCAAGGGGGA   GGATTGGGAA   GACAATAGCA

3301   GGCATGCTGG   GGATGCGGTG   GGCTCTATGG   CTTCTGAGGC   GGAAAGAACC

3351   AGCTGGGGCT   CTAGGGGGTA   TCCCCACGCG   CCCTGTAGCG   GCGCATTAAG

3401   CGCGGCGGGT   GTGGTGGTTA   CGCGCAGCGT   GACCGCTACA   CTTGCCAGCG

3451   CCCTAGCGCC   CGCTCCTTTC   GCTTTCTTCC   CTTCCTTTCT   CGCCACGTTC

3501   GCCGGGCCTC   TCAAAAAAGG   GAAAAAAAGC   ATGCATCTCA   ATTAGTCAGC

3551   AACCATAGTC   CCGCCCCTAA   CTCCGCCCAT   CCCGCCCCTA   ACTCCGCCCA

3601   GTTCCGCCCA   TTCTCCGCCC   CATGGCTGAC   TAATTTTTTT   TATTTATGCA

3651   GAGGCCGAGG   CCGCCTCGGC   CTCTGAGCTA   TTCCAGAAGT   AGTGAGGAGG

3701   CTTTTTTGGA   GGCCTAGGCT   TTTGCAAAAA   GCTTGGACAG   CTCAGGGCTG

3751   CGATTTCGCG   CCAAACTTGA   CGGCAATCCT   AGCGTGAAGG   CTGGTAGGAT

3801   TTTATCCCCG   CTGCCATCAT   GGTTCGACCA   TTGAACTGCA   TCGTCGCCGT

3851   GTCCCAAAAT   ATGGGGATTG   GCAAGAACGG   AGACCTACCC   TGGCCTCCGC

3901   TCAGGAACGA   GTTCAAGTAC   TTCCAAAGAA   TGACCACAAC   CTCTTCAGTG

3951   GAAGGTAAAC   AGAATCTGGT   GATTATGGGT   AGGAAAACCT   GGTTCTCCAT

4001   TCCTGAGAAG   AATCGACCTT   TAAAGGACAG   AATTAATATA   GTTCTCAGTA

4051   GAGAACTCAA   AGAACCACCA   CGAGGAGCTC   ATTTTCTTGC   CAAAAGTTTG

4101   GATGATGCCT   TAAGACTTAT   TGAACAACCG   GAATTGGCAA   GTAAAGTAGA

4151   CATGGTTTGG   ATAGTCGGAG   GCAGTTCTGT   TTACCAGGAA   GCCATGAATC

4201   AACCAGGCCA   CCTTAGACTC   TTTGTGACAA   GGATCATGCA   GGAATTTGAA

4251   AGTGACACGT   TTTTCCCAGA   AATTGATTTG   GGGAAATATA   AACTTCTCCC

4301   AGAATACCCA   GGCGTCCTCT   CTGAGGTCCA   GGAGGAAAAA   GGCATCAAGT
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FIGURE 18C (SEQ ID NO. 22)

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4351  ATAAGTTTGA AGTCTACGAG AAGAAAGACT AACAGGAAGA TGCTTTCAAG

4401  TTCTCTGCTC CCCTCCTAAA GCTATGCATT TTTATAAGAC CATGGGACTT

4451  TTGCTGGCTT TAGATCTCTT TGTGAAGGAA CCTTACTTCT GTGGTGTGAC

4501  ATAATTGGAC AAACTACCTA CAGAGATTTA AAGCTCTAAG GTAAATATAA

4551  AATTTTTAAG TGTATAATGT GTTAAACTAC TGATTCTAAT TGTTTGTGTA

4601  TTTTAGATTC CAACCTATGG AACTGATGAA TGGGAGCAGT GGTGGAATGC

4651  CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA TCTAGTGATG

4701  ATGAGGCTAC TGCTGACTCT CAACATTCTA CTCCTCCAAA AAAGAAGAGA

4751  AAGGTAGAAG ACCCCAAGGA CTTTCCTTCA GAATTGCTAA GTTTTTTGAG

4801  TCATGCTGTG TTTAGTAATA GAACTCTTGC TTGCTTTGCT ATTTACACCA

4851  CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA AAAATATTCT

4901  GTAACCTTTA TAAGTAGGCA TAACAGTTAT AATCATAACA TACTGTTTTT

4951  TCTTACTCCA CACAGGCATA GAGTGTCTGC TATTAATAAC TATGCTCAAA

5001  AATTGTGTAC CTTTAGCTTT TTAATTTGTA AAGGGGTTAA TAAGGAATAT

5051  TTGATGTATA GTGCCTTGAC TAGAGATCAT AATCAGCCAT ACCACATTTG

5101  TAGAGGTTTT ACTTGCTTTA AAAAACCTCC CACACCTCCC CCTGAACCTG

5151  AAACATAAAA TGAATGCAAT TGTTGTTGTT AACTTGTTTA TTGCAGCTTA

5201  TAATGGTTAC AAATAAAGCA ATAGCATCAC AAATTTCACA AATAAAGCAT

5251  TTTTTTCACT GCATTCTAGT TGTGGTTTGT CCAAACTCAT CAATGTATCT

5301  TATCATGTCT GGATCGGCTG GATGATCCTC CAGCGCGGGG ATCTCATGCT

5351  GGAGTTCTTC GCCCACCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA

5401  AATAAAGCAA TAGCATCACA AATTTCACAA ATAAAGCATT TTTTTCACTG

5451  CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG

5501  TATACCGTCG ACCTCTAGCT AGAGCTTGGC GTAATCATGG TCATAGCTGT

5551  TTCCTGTGTG AAATTGTTAT CCGCTCACAA TTCCACACAA CATACGAGCC

5601  GGAAGCATAA AGTGTAAAGC CTGGGGTGCC TAATGAGTGA GCTAACTCAC

5651  ATTAATTGCG TTGCGCTCAC TGCCCGCTTT CCAGTCGGGA AACCTGTCGT

5701  GCCAGCTGCA TTAATGAATC GGCCAACGCG CGGGGAGAGG CGGTTTGCGT

5751  ATTGGGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC GCTCGGTCGT

5801  TCGGCTGCGG CGAGCGGTAT CAGCTCACTC AAAGGCGGTA ATACGGTTAT
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FIGURE 18D (SEQ ID NO. 22)

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5851   CCACAGAATC AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG

5901   CAAAAGGCCA GGAACCGTAA AAAGGCCGCG TTGCTGGCGT TTTTCCATAG

5951   GCTCCGCCCC CCTGACGAGC ATCACAAAAA TCGACGCTCA AGTCAGAGGT

6001   GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC

6051   TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC

6101   CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCAATGC TCACGCTGTA

6151   GGTATCTCAG TTCGGTGTAG GTCGTTCGCT CCAAGCTGGG CTGTGTGCAC

6201   GAACCCCCCG TTCAGCCCGA CCGCTGCGCC TTATCCGGTA ACTATCGTCT

6251   TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA GCAGCCACTG

6301   GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG

6351   AAGTGGTGGC CTAACTACGG CTACACTAGA AGGACAGTAT TTGGTATCTG

6401   CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT

6451   CCGGCAAACA AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG

6501   CAGATTACGC GCAGAAAAAA AGGATCTCAA GAAGATCCTT TGATCTTTTC

6551   TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA GGGATTTTGG

6601   TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT AAATTAAAAA

6651   TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG

6701   TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTC

6751   GTTCATCCAT AGTTGCCTGA CTCCCCGTCG TGTAGATAAC TACGATACGG

6801   GAGGGCTTAC CATCTGGCCC CAGTGCTGCA ATGATACCGC GAGACCCACG

6851   CTCACCGGCT CCAGATTTAT CAGCAATAAA CCAGCCAGCC GGAAGGGCCG

6901   AGCGCAGAAG TGGTCCTGCA ACTTTATCCG CCTCCATCCA GTCTATTAAT

6951   TGTTGCCGGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA GTTTGCGCAA

7001   CGTTGTTGCC ATTGCTACAG GCATCGTGGT GTCACGCTCG TCGTTTGGTA

7051   TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC

7101   CCCATGTTGT GCAAAAAAGC GGTTAGCTCC TTCGGTCCTC CGATCGTTGT

7151   CAGAAGTAAG TTGGCCGCAG TGTTATCACT CATGGTTATG GCAGCACTGC

7201   ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT

7251   GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG

7301   CTCTTGCCCG GCGTCAATAC GGGATAATAC CGCGCCACAT AGCAGAACTT
```

FIGURE 18E (SEQ ID NO. 22)

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7351   TAAAAGTGCT CATCATTGGA AAACGTTCTT CGGGGCGAAA ACTCTCAAGG

7401   ATCTTACCGC TGTTGAGATC CAGTTCGATG TAACCCACTC GTGCACCCAA

7451   CTGATCTTCA GCATCTTTTA CTTTCACCAG CGTTTCTGGG TGAGCAAAAA

7501   CAGGAAGGCA AAATGCCGCA AAAAGGGAA TAAGGGCGAC ACGGAAATGT

7551   TGAATACTCA TACTCTTCCT TTTTCAATAT TATTGAAGCA TTTATCAGGG

7601   TTATTGTCTC ATGAGCGGAT ACATATTTGA ATGTATTTAG AAAAATAAAC

7651   AAATAGGGGT TCCGCGCACA TTTCCCCGAA AAGTGCCACC TGACGTCGAC

7701   GGATCGGGAG ATCTGCTAGG TGACCTGAGG CGCGCCGGCT TCGAATAGCC

7751   AGAGTAACCT TTTTTTTTAA TTTTATTTTA TTTTATTTTT GAGATGGAGT

7801   TTGGCGCCGA TCTCCCGATC CCCTATGGTC GACTCTCAGT ACAATCTGCT

7851   CTGATGCCGC ATAGTTAAGC CAGTATCTGC TCCCTGCTTG TGTGTTGGAG

7901   GTCGCTGAGT AGTGCGCGAG CAAAATTTAA GCTACAACAA GGCAAGGCTT

7951   GACCGACAAT TGCATGAAGA ATCTGCTTAG GGTTAGGCGT TTTGCGCTGC

8001   TTCGCGATGT ACGGGCCAGA TATACGCGTT GACATTGATT ATTGACTAGT

8051   TATTAATAGT AATCAATTAC GGGGTCATTA GTTCATAGCC CATATATGGA

8101   GTTCCGCGTT ACATAACTTA CGGTAAATGG CCCGCCTGGC TGACCGCCCA

8151   ACGACCCCCG CCCATTGACG TCAATAATGA CGTATGTTCC CATAGTAACG

8201   CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGACTATT TACGGTAAAC

8251   TGCCCACTTG GCAGTACATC AAGTGTATCA TATGCCAAGT ACGCCCCCTA

8301   TTGACGTCAA TGACGGTAAA TGGCCCGCCT GGCATTATGC CCAGTACATG

8351   ACCTTATGGG ACTTTCCTAC TTGGCAGTAC ATCTACGTAT TAGTCATCGC

8401   TATTACCATG GTGATGCGGT TTTGGCAGTA CATCAATGGG CGTGGATAGC

8451   GGTTTGACTC ACGGGGATTT CCAAGTCTCC ACCCCATTGA CGTCAATGGG

8501   AGTTTGTTTT GGCACCAAAA TCAACGGGAC TTTCCAAAAT GTCGTAACAA

8551   CTCCGCCCCA TTGACGCAAA TGGGCGGTAG GCGTGTACGG TGGGAGGTCT

8601   ATATAAGCAG AGCTCTCTGG CTAACTAGAG AACCCACTGC TTACTGGCTT

8651   ATCGAAATTA ATACGACTCA CTATAGGGAG ACCCAAGCTT
```

FIGURE 18F (SEQ ID NO. 22)

pD17-hG1b

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          10          20          30          40          50          60
GGTACCAATT  TAAATTGATA  TCTCCTTAGG  TCTCGAGTCT  CTAGATAACC  GGTCAATCGA
CCATGGTTAA  ATTTAACTAT  AGAGGAATCC  AGAGCTCAGA  GATCTATTGG  CCAGTTAGCT

          70          80          90         100         110         120
TTGGAATTCT  TGCGGCCGCT  TGCTAGCACC  AAGGGCCCAT  CGGTCTTCCC  CCTGGCACCC
AACCTTAAGA  ACGCCGGCGA  ACGATCGTGG  TTCCCGGGTA  GCCAGAAGGG  GGACCGTGGG

         130         140         150         160         170         180
TCCTCCAAGA  GCACCTCTGG  GGGCACAGCG  GCCCTGGGCT  GCCTGGTCAA  GGACTACTTC
AGGAGGTTCT  CGTGGAGACC  CCCGTGTCGC  CGGGACCCGA  CGGACCAGTT  CCTGATGAAG

         190         200         210         220         230         240
CCCGAACCGG  TGACGGTGTC  GTGGAACTCA  GGCGCCCTGA  CCAGCGGCGT  GCACACCTTC
GGGCTTGGCC  ACTGCCACAG  CACCTTGAGT  CCGCGGGACT  GGTCGCCGCA  CGTGTGGAAG

         250         260         270         280         290         300
CCGGCTGTCC  TACAGTCCTC  AGGACTCTAC  TCCCTCAGCA  GCGTGGTCAC  CGTGCCCTCC
GGCCGACAGG  ATGTCAGGAG  TCCTGAGATG  AGGGAGTCGT  CGCACCAGTG  GCACGGGAGG

         310         320         330         340         350         360
AGCAGCTTGG  GCACCCAGAC  CTACATCTGC  AACGTGAATC  ACAAGCCCAG  CAACACCAAG
TCGTCGAACC  CGTGGGTCTG  GATGTAGACG  TTGCACTTAG  TGTTCGGGTC  GTTGTGGTTC

         370         380         390         400         410         420
GTGGACAAGA  AAGTTGGTGA  GAGGCCAGCA  CAGGGAGGGA  GGGTGTCTGC  TGGAAGCCAG
CACCTGTTCT  TTCAACCACT  CTCCGGTCGT  GTCCCTCCCT  CCCACAGACG  ACCTTCGGTC

         430         440         450         460         470         480
GCTCAGCGCT  CCTGCCTGGA  CGCATCCCGG  CTATGCAGCC  CCAGTCCGAG  GCAGCAAGGC
CGAGTCGCGA  GGACGGACCT  GCGTAGGGCC  GATACGTCGG  GGTCAGGCTC  CGTCGTTCCG

         490         500         510         520         530         540
AGGCCCCGTC  TGCCTCTTCA  CCCGGAGGCC  TCTGCCCGCC  CCACTCATGC  TCAGGGAGAG
TCCGGGGCAG  ACGGAGAAGT  GGGCCTCCGG  AGACGGGCGG  GGTGAGTACG  AGTCCCTCTC

         550         560         570         580         590         600
GGTCTTCTGG  CTTTTTCCCC  AGGCTCTGGG  CAGGCACAGG  CTAGGTGCCC  CTAACCCAGG
CCAGAGACC   GAAAAAGGGG  TCCGAGACCC  GTCCGTGTCC  GATCCACGGG  GATTGGGTCC
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FIGURE 19B
(SEQ ID NO. 23)

pD17-hG1b

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    610        620        630        640        650        660
CCCTGCACAC AAAGGGGCAG GTGCTGGGCT CAGACCTGCC AAGAGCCATA TCCGGGAGGA
GGGACGTGTG TTTCCCCGTC CACGACCCGA GTCTGGACGG TTCTCGGTAT AGGCCCTCCT

    670        680        690        700        710        720
CCCTGCCCCT GACCTAAGCC CACCCCAAAG GCCAAACTCT CCACTCCCTC AGCTCGGACA
GGGACGGGGA CTGGATTCGG GTGGGGTTTC CGGTTTGAGA GGTGAGGGAG TCGAGCCTGT

    730        740        750        760        770        780
CCTTCTCTCC TCCCAGATTC CAGTAACTCC CAATCTTCTC TCTGCAGAGC CCAAATCTTG
GGAAGAGAGG AGGGTCTAAG GTCATTGAGG GTTAGAAGAG AGACGTCTCG GGTTTAGAAC

    790        800        810        820        830        840
TGACAAAACT CACACATGCC CACCGTGCCC AGGTAAGCCA GCCCAGGCCT CGCCCTCCAG
ACTGTTTTGA GTGTGTACGG GTGGCACGGG TCCATTCGGT CGGGTCCGGA GCGGGAGGTC

    850        860        870        880        890        900
CTCAAGGCGG GACAGGTGCC CTAGAGTAGC CTGCATCCAG GGACAGGCCC CAGCCGGGTG
GAGTTCCGCC CTGTCCACGG GATCTCATCG GACGTAGGTC CCTGTCCGGG GTCGGCCCAC

    910        920        930        940      950  237     960
CTGACACGTC CACCTCCATC TCTTCCTCAG CACCTGAACT  235 CTGTGGGGA CCGTCAGTCT
GACTGTGCAG GTGGAGGTAG AGAAGGAGTC GTGGACTTGA    GAC CCCCT  GGCAGTCAGA

    970        980        990        1000       1010       1020
TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT GAGGTCACAT
AGGAGAAGGG GGGTTTTGGG TTCCTGTGGG AGTACTAGAG GGCCTGGGGA CTCCAGTGTA

    1030       1040       1050       1060       1070       1080
GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG TACGTGGACG
CGCACCACCA CCTGCACTCG GTGCTTCTGG GACTCCAGTT CAAGTTGACC ATGCACCTGC

    1090       1100       1110       1120       1130       1140
GCCTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGGAGGA GCAGTACAAC AGCACGTACC
CGGACCTCCA CGTATTACGG TTCTGTTTCG GCGCCCCTCCT CGTCATGTTG TCGTGCATGG

    1150       1160       1170       1180       1190  318 320 1200
GTCTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGGCAAG GAGTACAAGT
CAGACCAGTC GCAGGAGTGG CAGGACGTGG TCCTGACCGA CTTACCCGTTC CTTCTGTTCA
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pD17-hG1b

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322 1210        1220        1230  331  1240        1250        1260
GCAGGTCTC  CAACAAAGCC  CTCCCAGCCC  CCATCGAGAA  AACCATCTCC  AAAGCCAAAG
CGTTCCAGAG  GTTGTTTCGG  GAGGGTCGGG  GGTAGCTCTT  TTGGTAGAGG  TTTCGGTTTC

1270        1280        1290        1300        1310        1320
GTGGGACCCG  TGGGGTGCGA  GGGCCACATG  GACAGAGGCC  GGCTCGGCCC  ACCCTCTGCC
CACCCTGGGC  ACCCCACGCT  CCCGGTGTAC  CTGTCTCCGG  CCGAGCCGGG  TGGGAGACGG

1330        1340        1350        1360        1370        1380
CTGAGAGTGA  CCGCTGTACC  AACCTCTGTC  CCTACAGGGC  AGCCCCGAGA  ACCACAGGTG
GACTCTCACT  GGCGACATGG  TTGGAGACAG  GGATGTCCCG  TCGGGGCTCT  TGGTGTCCAC

1390        1400        1410        1420        1430        1440
TACACCCTGC  CCCCATCCCG  GGATGAGCTG  ACCAAGAACC  AGGTCAGCCT  GACCTGCCTG
ATGTGGGACG  GGGGTAGGGC  CCTACTCGAC  TGGTTCTTGG  TCCAGTCGGA  CTGGACGGAC

1450        1460        1470        1480        1490        1500
GTCAAAGGCT  TCTATCCCAG  CGACATCGCC  GTGGAGTGGG  AGAGCAATGG  GCAGCCGGAG
CAGTTTCCGA  AGATAGGGTC  GCTGTAGCGG  CACCTCACCC  TCTCGTTACC  CGTCGGCCTC

1510        1520        1530        1540        1550        1560
AACAACTACA  AGACCACGCC  TCCCGTGCTG  GACTCCGACG  GCTCCTTCTT  CCTCTACAGC
TTGTTGATGT  TCTGGTGCGG  AGGGCACGAC  CTGAGGCTGC  CGAGGAAGAA  GGAGATGTCG

1570        1580        1590        1600        1610        1620
AAGCTCACCG  TGGACAAGAG  CAGGTGGCAG  CAGGGGAACG  TCTTCTCATG  CTCCGTGATG
TTCGAGTGGC  ACCTGTTCTC  GTCCACCGTC  GTCCCCTTGC  AGAAGAGTAC  GAGGCACTAC

1630        1640        1650        1660        1670        1680
CATGAGGCTC  TGCACAACCA  CTACACGCAG  AAGAGCCTCT  CCCTGTCTCC  GGGTAAATGA
GTACTCCGAG  ACGTGTTGGT  GATGTGCGTC  TTCTCGGAGA  GGGACAGAGG  CCCATTTACT

1690        1700        1710        1720        1730        1740
GTGCGACGGC  CGGCAAGCCC  CCGCTCCCCG  GGCTCTCGCG  GTCGCACGAG  GATGCTTGGC
CACGCTGCCG  GCCGTTCGGG  GGCGAGGGGC  CCGAGAGCGC  CAGCGTGCTC  CTACGAACCG

1750        1760        1770        1780        1790        1800
ACGTACCCCC  TGTACATACT  TCCCGGGCGC  CCAGCATGGA  AATAAAGCAC  CCAGCGCTGC
TGCCATGGGG  ACATGTATGA  AGGGCCCGCG  GGTCGTACCT  TTATTTCGTG  GGTCGCGACG
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FIGURE 19D
(SEQ ID NO. 23)

pD17-hG1b

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       1810             1820             1830             1840             1850             1860
CCTGGGCCCC   TGCGAGACTG   TGATGGTTCT   TTCCACGGGT   CAGGCCGAGT   CTGAGGCCTG
GGACCCGGGG   ACGCTCTGAC   ACTACCAAGA   AAGGTGCCCA   GTCCGGCTCA   GACTCCGGAC

       1870             1880             1890             1900             1910             1920
AGTGGCATGA   GGGAGGCAGA   GCGGGTCCCA   CTGTCCCCAC   ACTGGCCCAG   GCTGTGCAGG
TCACCGTACT   CCCTCCGTCT   CGCCCAGGGT   GACAGGGGTG   TGACCGGGTC   CGACACGTCC

       1930             1940             1950             1960             1970             1980
TGTGCCTGGG   CCCCCTAGGG   TGGGGCTCAG   CCAGGGGCTG   CCCTCGGCAG   GGTGGGGGAT
ACACGGACCC   GGGGGATCCC   ACCCCGAGTC   GGTCCCCGAC   GGGAGCCGTC   CCACCCCCTA

       1990             2000             2010             2020             2030             2040
TTGCCAGCGT   GGCCCTCCCT   CCAGCAGCAC   CTGCCCTGGG   CTGGGCCACG   GGAAGCCCTA
AACGGTCGCA   CCGGGAGGGA   GGTCGTCGTG   GACGGGACCC   GACCCGGTGC   CCTTCGGGAT

       2050             2060             2070             2080             2090             2100
GGAGCCCCTG   GGGACAGACA   CACAGCCCCT   GCCTCTGTAG   GAGACTGTCC   TGTTCTGTGA
CCTCGGGGAC   CCCTGTCTGT   GTGTCGGGGA   CGGAGACATC   CTCTGACAGG   ACAAGACACT

       2110             2120             2130             2140             2150             2160
GCGCCCCTGT   CCTCCCGACC   TCCATGCCCA   CTCGGGGGCA   TGCTGGGGAT   GCGGTGGGCT
CGCGGGGACA   GGAGGGCTGG   AGGTACGGGT   GAGCCCCCGT   ACGACCCCTA   CGCCACCCGA

       2170             2180             2190             2200             2210             2220
CTATGGCTTC   TGAGGCGGAA   AGAACCAGCT   GGGGCTCTAG   GGGGTATCCC   CACGGCGCCCT
GATACCGAAG   ACTCCGCCTT   TCTTGGTCGA   CCCCGAGATC   CCCCATAGGG   GTGCGCGGGA

       2230             2240             2250             2260             2270             2280
GTAGCGGCGC   ATTAAGCGCG   GCGGGTGTGG   TGGTTACGCG   CAGCGTGACC   GCTACACTTG
CATCGCCGCG   TAATTCGCGC   CGCCCACACC   ACCAATGCGC   GTCGCACTGG   CGATGTGAAC

       2290             2300             2310             2320             2330             2340
CCAGCGCCCT   AGCGCCCGCT   CCTTTCGCTT   TCTTCCCTTC   CTTTCTCGCC   ACGTTCGCCG
GGTCGCGGGA   TCGCGGGCGA   GGAAAGCGAA   AGAAGGGAAG   GAAAGAGCGG   TGCAAGCGGC

       2350             2360             2370             2380             2390             2400
GCTTTCCCCG   TCAAGCTCTA   AATCGGGGGCA   TCCCTTTAGG   GTTCCGATTT   AGTGCTTTAC
CGAAAGGGGC   AGTTCGAGAT   TTAGCCCCGT   AGGGAAATCC   CAAGGCTAAA   TCACGAAATG
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FIGURE 19E
(SEQ ID NO. 23)

pD17-hG1b

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        2410       2420       2430       2440       2450       2460
GGCACCTCGA CCCCAAAAAA CTTGATTAGG GTGATGGTTC ACGTAGTGGG CCATCGCCCT
CCGTGGAGCT GGGGTTTTTT GAACTAATCC CACTACCAAG TGCATCACCC GGTAGCGGGA

        2470       2480       2490       2500       2510       2520
GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT CTTTAATAGT GGACTCTTGT
CTATCTGCCA AAAAGCGGGA AACTGCAACC TCAGGTGCAA GAAATTATCA CCTGAGAACA

        2530       2540       2550       2560       2570       2580
TCCAAACTGG AACAACACTC AACCCTATCT CGGTCTATTC TTTTGATTTA TAAGGGATTT
AGGTTTGACC TTGTTGTGAG TTGGGATAGA GCCAGATAAG AAAACTAAAT ATTCCCTAAA

        2590       2600       2610       2620       2630       2640
TGGGGATTTC GGCCTATTGG TTAAAAAATG AGCTGATTTA ACAAAAATTT AACGCGAATT
ACCCCTAAAG CCGGATAACC AATTTTTTAC TCGACTAAAT TGTTTTTAAA TTGCGCTTAA

        2650       2660       2670       2680       2690       2700
AATTCTGTGG AATGTGTGTC AGTTAGGGTG TGGAAAGTCC CCAGGCTCCC CAGGCAGGCA
TTAAGACACC TTACACACAG TCAATCCCAC ACCTTTCAGG GGTCCGAGGG GTCCGTCCGT

        2710       2720       2730       2740       2750       2760
GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAT AGTCCCGCCC CTAACTCCGC
CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTTGGTA TCAGGGCGGG GATTGAGGCG

        2770       2780       2790       2800       2810       2820
CCATCCCGCC CCTAACTCCG CCCAGTTCCG CCCATTCTCC GCCCCATGGC TGACTAATTT
GGTAGGGCGG GGATTGAGGC GGGTCAAGGC GGGTAAGAGG CGGGGTACCG ACTGATTAAA

        2830       2840       2850       2860       2870       2880
TTTTTATTTA TGCAGAGGCC GAGGCCGCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG
AAAAATAAAT ACGTCTCCGG CTCCGGCGGA GCCGGAGACT CGATAAGGTC TTCATCACTC

        2890       2900       2910       2920       2930       2940
GAGGCTTTTT TGGAGGCCTA GGCTTTTGCA AAAAGCTTGG ACAGCTCAGG GCTGCGATTT
CTCCGAAAAA ACCTCCGGAT CCGAAAACGT TTTTCGAACC TGTCGAGTCC CGACGCTAAA

        2950       2960       2970       2980       2990       3000
CGCGCCAAAC TTGACGGCAA TCCTAGCCGTG AAGGCTGGTA GGATTTTATC CCCGCTGCCA
GCGCGGTTTG AACTGCCGTT AGGATCGCAC TTCCGACCAT CCTAAAATAG GGGCGACGGT
```

FIGURE 19F

(SEQ ID NO. 23)

pD17-hG1b

```
       3010       3020       3030       3040       3050       3060
TCATGGTTCG ACCATTGAAC TGCATCGTCG CCGTGTCCCA AAATATGGGG ATTGGCAAGA
AGTACCAAGC TGGTAACTTG ACGTAGCAGC GGCACAGGGT TTTATACCCC TAACCGTTCT

       3070       3080       3090       3100       3110       3120
ACGGAGACCT ACCCTGGCCT CCGCTCAGGA ACGAGTTCAA GTACTTCCAA AGAATGACCA
TGCCTCTGGA TGGGACCGGA GGCGAGTCCT TGCTCAAGTT CATGAAGGTT TCTTACTGGT

       3130       3140       3150       3160       3170       3180
CAACCTCTTC AGTGGAAGGT AAACAGAATC TGGTGATTAT GGGTAGGAAA ACCTGGTTCT
GTTGGAGAAG TCACCTTCCA TTTGTCTTAG ACCACTAATA CCCATCCTTT TGGACCAAGA

       3190       3200       3210       3220       3230       3240
CCATTCCTGA GAAGAATCGA CCTTTAAAGG ACAGAATTAA TATAGTTCTC AGTAGAGAAC
GGTAAGGACT CTTCTTAGCT GGAAATTTCC TGTCTTAATT ATATCAAGAG TCATCTCTTG

       3250       3260       3270       3280       3290       3300
TCAAAGAACC ACCACGAGGA GCTCATTTTC TTGCCAAAAG TTTGGATGAT GCCTTAAGAC
AGTTTCTTGG TGGTGCTCCT CGAGTAAAAG AACGGTTTTC AAACCTACTA CGGAATTCTG

       3310       3320       3330       3340       3350       3360
TTATTGAACA ACCGGAATTG GCAAGTAAAG TAGACATGGT TTGGATAGTC GGAGGCAGTT
AATAACTTGT TGGCCTTAAC CGTTCATTTC ATCTGTACCA AACCTATCAG CCTCCGTCAA

       3370       3380       3390       3400       3410       3420
CTGTTTACCA GGAAGCCATG AATCAACCAG GCCACCTTAG ACTCTTGTTG ACAAGGATCA
GACAAATGGT CCTTCGGTAC TTAGTTGGTC CGGTGGAATC TGAGAAACAC TGTTCCTAGT

       3430       3440       3450       3460       3470       3480
TGCAGGAATT TGAAAGTGAC ACGTTTTTCC CAGAAATTGA TTTGGGGAAA TATAAACTTC
ACGTCCTTAA ACTTTCACTG TGCAAAAAGG GTCTTTAACT AAACCCCTTT ATATTTGAAG

       3490       3500       3510       3520       3530       3540
TCCCAGAATA CCCAGCGCGTC CTCTCTGAGG TCCAGGAGGA AAAAGGCATC AAGTATAAGT
AGGGTCTTAT GGGTCCGCAG GAGAGACTCC AGGTCCTCCT TTTTCCGTAG TTCATATTCA

       3550       3560       3570       3580       3590       3600
TTGAAGTCTA CGAGAAGAAA GACTAACAGG AAGATGCTTT CAAGTTCTCT GCTCCCCTCC
AACTTCAGAT GCTCTTCTTT CTGATTGTCC TTCTACGAAA GTTCAAGAGA CGAGGGGAGG
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FIGURE 19G
(SEQ ID NO. 23)

pD17-hG1b

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       3610       3620       3630       3640       3650       3660
TAAAGCTATG CATTTTTATA AGACCATGGG ACTTTGCTG  GCTTTAGATC TCTTTGTGAA
ATTTCGATAC GTAAAAATAT TCTGGTACCC TGAAAACGAC CGAAATCTAG AGAAACACTT

       3670       3680       3690       3700       3710       3720
GGAACCTTAC TTCTGTGGTG TGACATAATT GGACAAACTA CCTACAGAGA TTTAAAGCTC
CCTTGGAATG AAGACACCAC ACTGTATTAA CCTGTTTGAT GGATGTCTCT AAATTTCGAG

       3730       3740       3750       3760       3770       3780
TAAGGTAAAT ATAAAATTTT TAAGTGTATA ATGTGTTAAA CTACTGATTC TAATTGTTTG
ATTCCATTTA TATTTTAAAA ATTCCACATAT TACACAATTT GATGACTAAG ATTAACAAAC

       3790       3800       3810       3820       3830       3840
TGTATTTTAG ATTCCAACCT ATGGAACTGA TGAATGGGAG CAGTGGTGGA ATGCCTTTAA
ACATAAAATC TAAGGTTGGA TACCTTGACT ACTTACCCTC GTCACCACCT TACGGAAATT

       3850       3860       3870       3880       3890       3900
TGAGGAAAAC CTGTTTTGCT CAGAAGAAAT GCCATCTAGT GATGATGAGG CTACTGCTGA
ACTCCTTTTG GACAAAACGA GTCTTCTTTA CGGTAGATCA CTACTACTCC GATGACGACT

       3910       3920       3930       3940       3950       3960
CTCTCAACAT TCTACTCCTC CAAAAAAGAA GAGAAAGGTA GAAGACCCCA AGGACTTTCC
GAGAGTTGTA AGATGAGGAG GTTTTTTCTT CTCTTTCCAT CTTCTGGGGT TCCTGAAAGG

       3970       3980       3990       4000       4010       4020
TTCAGAATTG CTAAGTTTTT TGAGTCATGC TGTGTTTAGT AATAGAACTC TTGCTTGCTT
AAGTCTTAAC GATTCAAAAA ACTCAGTACG ACACAAATCA TTATCTTGAG AACGAACGAA

       4030       4040       4050       4060       4070       4080
TGCTATTTAC ACCACAAAGG AAAAAGCTGC ACTGCTATAC AAGAAAAATTA TGGAAAAATA
ACGATAAATG TGGTGTTTCC TTTTTCGACG TGACGATATG TTCTTTTTAAT ACCTTTTTAT

       4090       4100       4110       4120       4130       4140
TTCTGTAACC TTTATAAGTA GGCATAACAG TTATAATCAT AACATACTGT TTTTTCTTAC
AAGACATTGG AAATATTCAT CCGTATTGTC AATATTAGTA TTGTATGACA AAAAAGAATG

       4150       4160       4170       4180       4190       4200
TCCACACAGG CATAGAGTGT CTGCTATTAA TAACTATGCT CAAAAATTGT GTACCTTTAG
AGGTGTGTCC GTATCTCACA GACGATAATT ATTGATACGA GTTTTAACA  CATGGAAATC
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FIGURE 19H
(SEQ ID NO. 23)

pD17-hG1b

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      4210       4220       4230       4240       4250       4260
CTTTTTAATT TGTAAAGGGG TTAATAAGGA ATATTTGATG TATAGTGCCT TGACTAGAGA
GAAAAATTAA ACATTTCCCC AATTATTCCT TATAAACTAC ATATCACGGA ACTGATCTCT

      4270       4280       4290       4300       4310       4320
TCATAATCAG CCATACCACA TTTGTAGAGG TTTTACTTGC TTTAAAAAAC CTCCCACACC
AGTATTAGTC GGTATGGTGT AAACATCTCC AAAATGAACG AAATTTTTTG GAGGGTGTGG

      4330       4340       4350       4360       4370       4380
TCCCCCTGAA CCTGAAACAT AAAATGAATG CAATTGTTGT TGTTAACTTG TTTTATTGCAG
AGGGGGACTT GGACTTTGTA TTTTACTTAC GTTAACAACA ACAATTGAAC AAATAACGTC

      4390       4400       4410       4420       4430       4440
CTTATAATGG TTACAAATAA AGCAATAGCA TCACAAATTT CACAAATAAA GCATTTTTTT
GAATATTACC AATGTTTATT TCGTTTATCGT AGTGTTTAAA GTGTTTATTT CGTAAAAAAA

      4450       4460       4470       4480       4490       4500
CACTGCATTC TAGTTGTGGT TTGTCCAAAC TCATCAATGT ATCTTATCAT GTCTGGATCG
GTGACGTAAG ATCACACCA AACAGGTTTG AGTAGTTACA TAGAATAGTA CAGACCTAGC

      4510       4520       4530       4540       4550       4560
GCTGGATGAT CCTCCAGCGC GGGGATCTCA TGCTGGAGTT CTTCGCCCAC CCCAACTTGT
CGACCTACTA GGAGGTCGCG CCCCTAGAGT ACGACCTCAA GAAGCGGGTG GGGTTGAACA

      4570       4580       4590       4600       4610       4620
TTATTGCAGC TTATAATGGT TACAAATAAA GCAATAGCAT CACAAATTTC ACAAATAAAG
AATAACGTCG AATATTACCA ATGTTTATTT CGTTATCGTA GTGTTTAAAG TGTTTATTTC

      4630       4640       4650       4660       4670       4680
CATTTTTTTC ACTGCATTCT AGTTGTGGTT TGTCCAAACT CATCAATGTA TCTTATCATG
GTAAAAAAAG TGACGTAAGA TCAACACCAA ACAGGTTTGA GTAGTTACAT AGAATAGTAC

      4690       4700       4710       4720       4730       4740
TCTGTATACC GTCGACCTCT AGCTAGAGCT TGGCGTAATC ATGGTCATAG CTGTTTCCTG
AGACATATGG CAGCTGGAGA TCGATCTCGA ACCGCATTAG TACCAGTATC GACAAAGGAC

      4750       4760       4770       4780       4790       4800
TGTGAAATTG TTATCCGCTC ACAATTCCAC ACAACATACG AGCCGGAAGC ATAAAGTGTA
ACACTTTAAC AATAGGCGAG TGTTAAGGTG TGTTGTATGC TCGGCCTTCG TATTTCACAT
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FIGURE 19I
(SEQ ID NO. 23)

pD17-hG1b

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        4810       4820       4830       4840       4850       4860
AAGCCTGGGG TGCCTAATGA GTGAGCTAAC TCACATTAAT TGCGTTGCGC TCACTGCCCG
TTCGGACCCC ACGGATTACT CACTCGATTG AGTGTAATTA ACGCAACGCG AGTGACGGGC

        4870       4880       4890       4900       4910       4920
CTTTCCAGTC GGGAAACCTG TCGTGCCAGC TGCATTAATG AATCGGCCAA CGGCGGGGGA
GAAAGGTCAG CCCTTTGGAC AGCACGGTCG ACGTAATTAC TTAGCCGGTT GCGCGCCCCT

        4930       4940       4950       4960       4970       4980
GAGGCGGTTT GCGTATTGGG CGCTCTTCCG CTTCCTCGCT CACTGACTCG CTGCGCTCGG
CTCCGCCAAA CGCATAACCC GCGAGAAGGC GAAGGAGCGA GTGACTGAGC GACGCGAGCC

        4990       5000       5010       5020       5030       5040
TCGTTCGGCT GCGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAATACGG TTATCCACAG
AGCAAGCCGA CGCCGCTCGC CATAGTCGAG TGAGTTTCCG CCATTATGCC AATAGGTGTC

        5050       5060       5070       5080       5090       5100
AATCAGGGGA TAACGCAGGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG GCCAGGAACC
TTAGTCCCCT ATTGCGTCCT TTCTTGTACA CTCGTTTTCC GGTCGTTTTC CGGTCCTTGG

        5110       5120       5130       5140       5150       5160
GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC ATAGGCTCCG CCCCCCTGAC GAGCATCACA
CATTTTTCCG GCGCAACGAC CGCAAAAAGG TATCCGAGGC GGGGGGACTG CTCGTAGTGT

        5170       5180       5190       5200       5210       5220
AAAATCGACG CTCAAGTCAG AGGTGGCGAA ACCCGACAGG ACTATAAAGA TACCAGGCGT
TTTTAGCTGC GAGTTCAGTC TCCACCGCTT TGGGCTGTCC TGATATTTCT ATGGTCCGCA

        5230       5240       5250       5260       5270       5280
TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC
AAGGGGGACC TTCGAGGGAG CACGCGAGAG GACAAGGCTG GGACGGCGAA TGGCCTATGG

        5290       5300       5310       5320       5330       5340
TGTCCGCCTT TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA ATGCTCACGC TGTAGGTATC
ACAGGCGGAA AGAGGGAAGC CCTTCGCACC GCGAAAGAGT TACGAGTGCG ACATCCATAG

        5350       5360       5370       5380       5390       5400
TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC CCCGTTCAGC
AGTCAAGCCA CATCCAGCAA GCGAGGTTCG ACCCGACACA CGTGCTTGGG GGGCAAGTCG
```

FIGURE 19J
(SEQ ID NO. 23)

pD17-hG1b

```
       5410       5420       5430       5440       5450       5460
CCGACCGCTG CGCCTTATCC GGTAACTATC GTCTTGAGTC CAACCCGGTA AGACACGACT
GGCTGGCGAC GCGGAATAGG CCATTGATAG CAGAACTCAG GTTGGGCCAT TCTGTGCTGA

       5470       5480       5490       5500       5510       5520
TATCGCCACT GGCAGCAGCC ACTGGTAACA GGATTAGCAG AGCGAGGTAT GTAGGCGGTG
ATAGCGGTGA CCGTCGTCGG TGACCATTGT CCTAATCGTC TCGCTCCATA CATCCGCCAC

       5530       5540       5550       5560       5570       5580
CTACAGAGTT CTTGAAGTGG TGGCCTAACT ACGGCTACAC TAGAAGGACA GTATTTGGTA
GATGTCTCAA GAACTTCACC ACCGGATTGA TGCCGATGTG ATCTTCCTGT CATAAACCAT

       5590       5600       5610       5620       5630       5640
TCTGCGCTCT GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA
AGACGCGAGA CGACTTCGGT CAATGGAAGC CTTTTTCTCA ACCATCGAGA ACTAGGCCGT

       5650       5660       5670       5680       5690       5700
AACAAACCAC CGCTGGTAGC GGTGGTTTTT TTGTTTGCAA GCAGCAGATT ACGGGCAGAA
TTGTTTGGTG GCGACCATCG CCACCAAAAA AACAAACGTT CGTCGTCTAA TGCGCGTCTT

       5710       5720       5730       5740       5750       5760
AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG GTCTGACGCT CAGTGGAACG
TTTTTCCTAG AGTTCTTCTA GGAAACTAGA AAAGATGCCC CAGACTGCGA GTCACCTTGC

       5770       5780       5790       5800       5810       5820
AAAACTCACG TTAAGGGATT TTGGTCATGA GATTATCAAA AAGGATCTTC ACCTAGATCC
TTTTGAGTGC AATTCCCTAA AACCAGTACT CTAATAGTTT TTCCTAGAAG TGGATCTAGG

       5830       5840       5850       5860       5870       5880
TTTAAATTA AAAATGAAGT TTTAAATCAA TCTAAAGTAT ATATGAGTAA ACTTGGTCTG
AAAATTTAAT TTTTACTTCA AAATTTAGTT AGATTTCATA TATACTCATT TGAACCAGAC

       5890       5900       5910       5920       5930       5940
ACAGTTACCA ATGCTTAATC AGTGAGGCAC CTATCCTCAGC GATCTGTCTA TTTCGTTCAT
TGTCAATGGT TACGAATTAG TCACTCCGTG GATAGAGTCG CTAGACAGAT AAAGCAAGTA

       5950       5960       5970       5980       5990       6000
CCATAGTTGC CTGACTCCCC GTCGTGTAGA TAACTACGAT ACGGGAGGGC TTACCATCTG
GGTATCAACG GACTGAGGGG CAGCACATCT ATTGATGCTA TGCCCTCCCG AATGGTAGAC
```

FIGURE 19K
(SEQ ID NO. 23)

pD17-hG1b

```
6010        6020        6030        6040        6050        6060
GCCCCAGTGC  TGCAATGATA  CCCGGAGACC  CACGCTCACC  GGCTCCAGAT  TTATCAGCAA
CGGGGTCACG  ACGTTACTAT  GGGCGCTCTGG GTGCGAGTGG  CCGAGGTCTA  AATAGTCGTT

6070        6080        6090        6100        6110        6120
TAAACCAGCC  AGCCGGAAGG  GCCGAGCGCA  GAAGTGGTCC  TGCAACTTTA  TCCGCCTCCA
ATTTGGTCGG  TCGGCCTTCC  CGGCTCGCGT  CTTCACCAGG  ACGTTGAAAT  AGGCGGAGGT

6130        6140        6150        6160        6170        6180
TCCAGTCTAT  TAATTGTTGC  CGGGAAGCTA  GAGTAAGTAG  TTCGCCAGTT  AATAGTTTGC
AGGTCAGATA  ATTAACAACG  GCCCTTCGAT  CTCATTCATC  AAGCGGTCAA  TTATCAAACG

6190        6200        6210        6220        6230        6240
GCAACGTTGT  TGCCATTGCT  ACAGGCATCG  TGGTGTCACG  CTCGTCGTTT  GGTATGGCTT
CGTTGCAACA  ACGGTAACGA  TGTCCGTAGC  ACCACAGTGC  GAGCAGCAAA  CCATACCGAA

6250        6260        6270        6280        6290        6300
CATTCAGCTC  CGGTTCCCAA  CGATCAAGGC  GAGTTACATG  ATCCCCCATG  TTGTGCAAAA
GTAAGTCGAG  GCCAAGGGTT  GCTAGTTCCG  CTCAATGTAC  TAGGGGGTAC  AACACGTTTT

6310        6320        6330        6340        6350        6360
AAGCGGTTAG  CTCCTTCGGT  CCTCCGATCG  TTGTCAGAAG  TAAGTTGGCC  GCAGTGTTAT
TTCGCCAATC  GAGGAAGCCA  GGAGGCTAGC  AACAGTCTTC  ATTCAACCGG  CGTCACAATA

6370        6380        6390        6400        6410        6420
CACTCATGGT  TATGGCAGCA  CTGCATAATT  CTCTTACTGT  CATGCCCATCC GTAAGATGCT
GTGAGTACCA  ATACCGTCGT  GACGTATTAA  GAGAATGACA  GTACGGTAGG  CATTCTACGA

6430        6440        6450        6460        6470        6480
TTTCTGTGAC  TGGTGAGTAC  TCAACCAAGT  CATTCTGAGA  ATAGTGTATG  CGGCGACCGA
AAAGACACTG  ACCACTCATG  AGTTGGTTCA  GTAAGACTCT  TATCACATAC  GCCGCTGGCT

6490        6500        6510        6520        6530        6540
GTTGCTCTTG  CCCGGGCGTCA ATACGGGGATA ATACCCGCGCC ACATAGCAGA  ACTTTAAAAG
CAACGAGAAC  GGGCCGCAGT  TATGCCCCTAT TATGGCGCGG  TGTATCGTCT  TGAAATTTTC

6550        6560        6570        6580        6590        6600
TGCTCATCAT  TGGAAAACGT  TCTTCGGGGC  GAAAACTCTC  AAGGATCTTA  CCGGTGTTGA
ACGAGTAGTA  ACCTTTTGCA  AGAAGCCCCG  CTTTTGAGAG  TTCCTAGAAT  GGCCGACAACT
```

pD17-hG1b

```
            6610        6620        6630        6640        6650        6660
      GATCCCAGTTC  GATGTAACCC  ACTCGTGCAC  CCAACTGATC  TTCAGCATCT  TTTACTTTCA
      CTAGGGTCAAG  CTACATTGGG  TGAGCACGTG  GGTTGACTAG  AAGTCGTAGA  AAATGAAAGT

            6670        6680        6690        6700        6710        6720
      CCAGCGTTTC  TGGGTGAGCA  AAAACAGGAA  GGCAAAATGC  CGCAAAAAAG  GGAATAAGGG
      GGTCGCAAAG  ACCCACTCGT  TTTTGTCCTT  CCGTTTTACG  GCGTTTTTTC  CCTTATTCCC

            6730        6740        6750        6760        6770        6780
      CGACACGGAA  ATGTTGAATA  CTCATACTCT  TCCTTTTTCA  ATATTATTGA  AGCATTTATC
      GCTGTGCCTT  TACAACTTAT  GAGTATGAGA  AGGAAAAAGT  TATAATAACT  TCGTAAATAG

            6790        6800        6810        6820        6830        6840
      AGGGTTATTG  TCTCATGAGC  GGATACATAT  TTGAATGTAT  TTAGAAAAAT  AAACAAATAG
      TCCCAATAAC  AGAGTACTCG  CCTATGTATA  AACTTACATA  AATCTTTTTA  TTTGTTTATC

            6850        6860        6870        6880        6890        6900
      GGGTTCCGCG  CACATTTCCC  CGAAAAGTGC  CACCTGACGT  CGACGGATCG  GGAGATCTGC
      CCCAAGGCGC  GTGTAAAGGG  GCTTTTCACG  GTGGACTGCA  GCTGCCTAGC  CCTCTAGACG

            6910        6920        6930        6940        6950        6960
      TAGGTGACCT  GAGGCGCGCC  GGCTTCGAAT  AGCCAGAGTA  ACCTTTTTTT  TTAATTTTAT
      ATCCACTGGA  CTCCGCGCGG  CCGAAGCTTA  TCGGTCTCAT  TGGAAAAAAA  AATTAAAATA

            6970        6980        6990        7000        7010        7020
      TTTATTTTAT  TTTTGAGATG  GAGTTTTGCG  CCGATCTCCC  GATCCCCTAT  GGTCGACTCT
      AAATAAAATA  AAAACTCTAC  CTCAAAACGC  GGCTAGAGGG  CTAGGGGATA  CCAGCTGAGA

            7030        7040        7050        7060        7070        7080
      CAGTACAATC  TGCTCTGATG  CCGCATAGTT  AAGCCAGTAT  CTGCTCCCTG  CTTGTGTGTT
      GTCATGTTAG  ACGAGACTAC  GGCGTATCAA  TTCGGTCATA  GACGAGGGAC  GAACACACAA

            7090        7100        7110        7120        7130        7140
      GGAGGTCGCT  GAGTAGTGCG  CGAGCAAAAT  TTAAGCTACA  ACAAGGCAAG  GCTTGACCGA
      CCTCCAGCGA  CTCATCACGC  GCTCGTTTTA  AATTCGATGT  TGTTCCGTTC  CGAACTGGCT

            7150        7160        7170        7180        7190        7200
      CAATTGCATG  AAGAATCTGC  TTAGGGTTAG  GCGTTTGCCG  CTGCTTCGCG  ATGTACGGGC
      GTTAACGTAC  TTCTTAGACG  AATCCCAATC  CGCAAACGGC  GACGAAGCGC  TACATGCCCG
```

FIGURE 19M

(SEQ ID NO. 23)

pD17-hG1b

```
      7210       7220       7230       7240       7250       7260
CAGATATACG CGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC
GTCTATATGC GCAACTGTAA CTAATAACTG ATCAATAATT ATCATTAGTT AATGCCCCAG

      7270       7280       7290       7300       7310       7320
ATTAGTTCAT AGCCCATATA TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC
TAATCAAGTA TCGGGTATAT ACCTCAAGGC GCAATGTATT GAATGCCATT TACCGGGCGG

      7330       7340       7350       7360       7370       7380
TGGCTGACCG CCCAACGACC CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT
ACCGACTGGC GGGTTGCTGG GGGCGGGTAA CTGCAGTTAT TACTGCATAC AAGGGTATCA

      7390       7400       7410       7420       7430       7440
AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAC TATTTACGGT AAACTGCCCA
TTGCGGTTAT CCCTGAAAGG TAACTGCAGT TACCCACCTG ATAAATGCCA TTTGACGGGT

      7450       7460       7470       7480       7490       7500
CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCCC CCTATTGACG TCAATGACGG
GAACCGTCAT GTAGTTCACA TAGTATACGG TTCATGCGGG GGATAACTGC AGTTACTGCC

      7510       7520       7530       7540       7550       7560
TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA
ATTTACCGGG CGGACCGTAA TACGGGTCAT GTACTGGAAT ACCCTGAAAG GATGAACCGT

      7570       7580       7590       7600       7610       7620
GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA
CATGTAGATG CATAATCAGT AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT

      7630       7640       7650       7660       7670       7680
TGGGCGTGGA TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
ACCCGCACCT ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

      7690       7700       7710       7720       7730       7740
TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC
ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT TGTTGAGGCG

      7750       7760       7770       7780       7790       7800
CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT
GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC CAGATATATT CGTCTCGAGA
```

FIGURE 19N

(SEQ ID NO. 23)

pD17-hG1b

```
        7810       7820       7830       7840       7850       7860
CTGGCTAACT AGAGAACCCA CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG
GACCGATTGA TCTCTTGGGT GACGAATGAC CGAATAGCTT TAATTATGCT GAGTGATATC

        7870       7880
GGAGACCCAA GCTT
CCTCTGGGTT CGAA
```

Figure 26

hBR96-2 Heavy Chain Variable Region (V$_H$)

```
1              11             21             31             41
EVQLVESGGG LVQPGGSLRL SCAASGFPFS DYYMYWVRQA PGKGLEWVSY
51         61             71             81             91
ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL
101            111
ADGAWFAYWG QGTLVTVSS   (SEQ ID NO. 24)
```

human IgG1 constant

```
           |CH1
           A STKGPSVFPL APSSKSTSGG TAALGCLVKD

YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY

ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP C|CH2 235 237
                                  P APEILLGGP SVFLFPPKPK

DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS
                      318 320 322          334
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV
                                            |CH3

YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL

DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK
```

(SEQ ID NO. 25)

Figure 27

hBR96-2A: Heavy Chain Variable Region (V$_H$)

```
 1          11          21          31          41
EVQLVESGGG LVQPGGSLRL SCAASGFPFS DYYMYWVRQA PGKGLEWVSY

51         61          71          81          91
ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL

101        111
ADGAWFAYWG QGTLVTVSS (SEQ ID NO. 24)
```

hBR96-2A: Human Heavy Chain IgG1 Constant Region ΔCH2

```
A STKGPSVFPL APSSKSTSGG TAALGCLVKD YFPEPVTVSW NSGALTSGVH

TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK

SCDKTHTCPP CP   GQPREPQV YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA

VEWESNGQPE NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM

HEALHNHYTQ KSLSLSPGK (SEQ ID NO. 26)
```

Figure 28

This sequence is the [chi BR96 IgG1 with CH2 deleted.]

VH
```
  1  EVNLVESGGG LVQPGGSLKV SCVTSGFTFS DYYMYWVRQT PEKRLEWVAY

 51  ISQGGDITDY PDTVKGRFTI SRDNAKNTLY LQMSRLKSED TAMYYCARGL

                      CH1
101  DDGAWFAYWG QGTLVTVSVA STKGPSVFPL APSSKSTSGG TAALGCLVKD

151  YPPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY

                                          CH3
201  ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CHGQPREPQV YTLPPSRDEL

251  TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS

301  KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK
```

(SEQ ID NO. 27)